

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

(51) International Patent Classification ⁶ : A01N 63/02, 63/00		A1	(11) International Publication Number: WO 97/46105
			(43) International Publication Date: 11 December 1997 (11.12.97)
(21) International Application Number: PCT/EP97/02737 (22) International Filing Date: 27 May 1997 (27.05.97) (30) Priority Data: 9611777.5 6 June 1996 (06.06.96) GB (71) Applicant (for all designated States except US): NOVARTIS AG [CH/CH]; Schwarzwaldallee 215, CH-4058 Basel.(CH). (72) Inventors; and (75) Inventors/Applicants (for US only): SUWANTARADON, Kriangsak [TH/TH]; 59/143 Senaniwes Village 2, Soi Senanikom 1, Ladprao, Bangkok 10230 (TH). HUNTER, Bruce [CA/CA]; R.R. #5, Guelph, Ontario N1H 6J2 (CA). UITDEWILLIGEN, Wilhelmus, Petrus, Maria [BR/BR]; Edificio San Marco, Apartamento 1700, Rua Rafael Rinaldi 281, CEP-38401-097 Uberlandia, MG (BR). (74) Agent: ROTH, Bernhard, M.; Novartis AG, Patent- und Markenabteilung, Klybeckstrasse 141, CH-4002 Basel (CH).		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>	
(54) Title: METHOD OF CONTROLLING INSECT PESTS			
(57) Abstract			
The present invention provides a method of controlling <i>Ostrinia furnacalis</i> (Asian Corn Borer) species in crop plants, but especially in maize and other cereal plants, including, but not limited to the following species of plants: maize, wheat, barley, rye, oats, rice, sorghum, millet and related crops, forage grasses, bamboo and sugar cane.			
BEST AVAILABLE COPY			

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakhstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

Method of Controlling Insect Pests

The present invention relates to a method of controlling species of the Lepidoptera genus *Ostrinia* species preferably *Ostrinia furnacalis* (*Asian Corn Borer*), in crop plants by use of toxin proteins obtainable from *Bacillus thuringiensis* and/or other *Bacillus* species.

Bacillus thuringiensis belongs to the large group of gram-positive, aerobic, endospore-forming bacteria. Unlike other very closely related species of *Bacillus* such as *B. cereus* or *B. anthracis*, the majority of the hitherto known *Bacillus thuringiensis* species produce in the course of their sporulation a parasporal inclusion body which, due to its crystalline structure, is generally referred to as a crystalline body. This crystalline body is composed of insecticidally active crystalline protoxin proteins, the so-called δ -endotoxins.

The protein crystals are responsible for the toxicity to insects of *Bacillus thuringiensis*. The δ -endotoxin does not exhibit its insecticidal activity until after oral ingestion of the crystalline body, when the latter is dissolved in the intestinal juice of the target insects. In most cases the actual toxic component is released from the protoxin as a result of proteolytic cleavage caused by the action of proteases from the digestive tract of the insects.

The δ -endotoxins of the various *Bacillus thuringiensis* strains are characterized by high specificity toward certain target insects, especially with respect to various Lepidoptera, Coleoptera and Diptera larvae, and by a high degree of activity against such susceptible larvae. A further advantage of *Bacillus thuringiensis* δ -endotoxins resides in the fact that the toxins are harmless to humans, other mammals, birds and fish.

The various insecticidal crystal proteins from *Bacillus thuringiensis* have been classified based upon their spectrum of activity and sequence similarity. The classification put forth by Höfte and Whiteley, Microbiol. Rev. 53: 242-255 (1989) placed the then known insecticidal crystal proteins into four major classes. Generally, the major classes are defined by their spectrum of activity, with the CryI proteins being active against Lepidoptera, CryII proteins against both Lepidoptera and Diptera, CryIII proteins being active against Coleoptera, and CryIV proteins against Diptera.

Within each major class, the δ -endotoxins are grouped according to sequence similarity.

The CryI proteins are typically produced as 130-140 kDa protoxin proteins which are proteolytically cleaved to produce insecticidally active toxin proteins about 60-70 kDa

- 2 -

in size. The active portion of a δ -endotoxin resides in the NH_2 -terminal portion of the full-length molecule. Höfte and Whiteley, *supra*, classified the then known CryI proteins into six groups, IA(a), IA(b), IA(c), IB, IC, and ID. Since then, proteins classified as CryIE, CryIF, CryIG, CryIH and CryIX have also been characterized.

The spectrum of insecticidal activity of an individual δ -endotoxin from *Bacillus thuringiensis* tends to be quite narrow, with a given δ -endotoxin being active against only a few insects. Specificity is the result of the efficiency of the various steps involved in producing an active toxin protein and its subsequent ability to interact with the epithelial cells in the insect digestive tract.

It is one of the objects of this invention to provide a method of controlling *Ostrinia furnacalis* (Asian Corn Borer) species in plants, preferably cereal crops, including, but not limited to the species of maize, wheat, rye, oats, rice, sorghum, millet and related crops, forage grasses, bamboo and sugar cane. This object could surprisingly be achieved within the scope of the invention by administering a toxin protein of *Bacillus thuringiensis* such as a CryI-type toxin protein, to the crop plant to be protected. In another embodiment of the invention toxin proteins obtainable from vegetative cultures of *Bacillus* species, so-called Vegetative Insecticidal Proteins (VIPs) such as VIP3 [EP-A 0 690 916; International Application no EP95/03826, the disclosure of which is incorporated herein by reference in its entirety], can also be used to control *Ostrinia furnacalis* (Asian Corn Borer) pests.

The present invention thus relates to a method for protecting plants including progeny thereof against damage caused by *Ostrinia furnacalis* (Asian Corn Borer) species comprising directly or indirectly administering to the plant or the plant seed or the growing area of the plant to be protected a toxin protein of *Bacillus* species, preferably a CryI-type or a VIP-type protein mentioned above, either purely or in the form of an entomocidal composition comprising at least one of said proteins or a microorganism, preferably a *Bacillus thuringiensis* and/or a *Bacillus cereus* strain, containing at least one toxin gene encoding the toxin protein. Said microorganisms used in the method according to the invention may either be naturally occurring strains or, in the alternative, recombinant strains comprising a recombinant gene encoding the toxin.

In a preferred embodiment, transgenic plants are used to administer the toxin to the plants to be protected against damage caused by *Ostrinia furnacalis* (Asian Corn

Borer) species. Such plants are obtained by transformation with a toxin gene encoding an insecticidal toxin protein from a *Bacillus* species such as a Cry-type, preferably a CryI-type toxin protein or a VIP-type protein, and expressing said toxin protein in an amount sufficient to provide control against *Ostrinia furnacalis* (*Asian Corn Borer*) species upon planting the so transformed plant in an area where said insect pest occurs.

Entomocidal compositions to be used in the method according to the invention for protecting crop plants against *Ostrinia furnacalis* (*Asian Corn Borer*) pests for example comprise as an active ingredient at least one Cry-type toxin protein, more preferred at least one CryI-type toxin protein, even more preferred at least one CryIA-type toxin protein, particularly preferred at least one CryIA(b)-type toxin protein and most particularly preferred at least one cryIA(b) type toxin protein according to SEQ ID NOS: 53 to 55, even more preferred of *Bacillus thuringiensis* or a microorganism containing at least one gene encoding said toxin protein, preferably a *Bacillus thuringiensis* strain containing at least one gene encoding said toxin protein, or a derivative or mutant thereof, together with an agricultural adjuvant such as a carrier, diluent, surfactant or application-promoting adjuvant. The active ingredient contained in the entomocidal composition may also be a VIP-type toxin protein as disclosed in EP-A- 0 690 916 and the PCT International Application No EP95/03826 or a combination of CryI-type and VIP-type proteins. Preferred within the scope of protection is aVIP1-type protein, such as a VIP1A(a) protein or a VIP1A(b) protein, or a VIP2- type protein, such as a VIP2A(a) protein or a VIP2A(b) protein or a combination of a VIP1-type protein and a VIP2-type protein or aVIP3-type protein, such as a VIP3A(a) protein or a VIP3A(b) protein.

More preferred within the scope of protection are VIP-type toxin proteins as shown in SEQ ID NOS: 1, 2, 4-7, 17-24, 26-32, 35, 36, 39, 40, 42, 43, 45, 46, 49, 50, 51 or 52.

The composition may also contain a further biologically active compound. Said compound can be both a fertilizer or micronutrient donor or other preparations that influence plant growth. It can also be a selective herbicide, insecticide, fungicide, bactericide, nematocide, molluscicide or mixtures of several of these preparations, if desired, together with further agriculturally acceptable carriers, surfactants or application-promoting adjuvants customarily employed in the art of formulation. Suitable carriers and adjuvants can be solid or liquid and correspond to the substances ordinarily

employed in formulation technology, e.g. natural or regenerated mineral substances, solvents, dispersants, wetting agents, tackifiers, binders or fertilizers.

The composition may comprise from 0.1 to 99% by weight of the active ingredient, from 1 to 99.9% by weight of a solid or liquid adjuvant, and from 0 to 25% by weight of a surfactant. The active ingredient or the composition containing said active ingredient, may be administered to the plants or crops to be protected together with certain other insecticides or chemicals (1993 Crop Protection Chemicals Reference, Chemical and Pharmaceutical Press, Canada) without loss of potency. It is compatible with most other commonly used agricultural spray materials but should not be used in extremely alkaline spray solutions if a CryI-type toxin is involved. It may be administered as a dust, a suspension, a wettable powder or in any other material form suitable for agricultural application.

The active ingredient, that is preferably a CryI-type toxin protein of *Bacillus thuringiensis* and/or one of the VIP-type proteins mentioned previously, or the composition comprising said active ingredient may be applied to (a) an environment in which the insect pest may occur, (b) a plant or plant part in order to protect said plant or plant part from damage caused by an insect pest, or (c) seed in order to protect a plant which develops from said seed from damage caused the pest.

A preferred method of application in the area of plant protection is application to the foliage of the plants (foliar application), with the number of applications and the rate of application depending on the plant to be protected and the risk of infestation by the pest in question.

The compositions to be used in a method according to the invention are also suitable for protecting plant propagating material, e.g. seed, such as fruit, tubers or grains, or plant cuttings, from insect pests. The propagation material can be treated with the formulation before planting: seed, for example, can be dressed before being sown. The active ingredient of the invention can also be applied to grains (coating), either by impregnating the grains with a liquid formulation or by coating them with a solid formulation. The formulation can also be applied to the planting site when the propagating material is being planted, for example to the seed furrow during sowing. The invention relates also to those methods of treating plant propagation material and to the plant propagation material thus treated.

Within the scope of the invention the compositions may be applied in any method known for treatment of seed or soil with bacterial strains. For example, see US Patent No.4,863,866. The strains are effective for biocontrol even if the microorganism is not living. Preferred is, however, the application of the living microorganism.

Target crops to be protected within the scope of the present invention are those that are host plants for *Ostrinia furnacalis* (*Asian Corn Borer*) species and include but are not limited to the species of maize, wheat, barley, rye, oats, rice, sorghum, millet and related crops, forage grasses, bamboo and sugar cane.

The active ingredient according to the invention may be used in unmodified form or together with any suitable agriculturally acceptable carrier. Such carriers are adjuvants conventionally employed in the art of agricultural formulation, and are therefore formulated in known manner to emulsifiable concentrates, coatable pastes, directly sprayable or dilutable solutions, dilute emulsions, wettable powders, soluble powders, dusts, granulates, and also encapsulations, for example, in polymer substances. Like the nature of the compositions, the methods of application, such as spraying, atomizing, dusting, scattering or pouring, are chosen in accordance with the intended objective and the prevailing circumstances. Advantageous rates of application range from about 50 g to about 5 kg of active ingredient (a.i.) per hectare ("ha", approximately 2.471 acres), and preferably from about 100 g to about 2 kg a.i./ha. Preferred rates of application are 200 g to about 1 kg a.i./ha or 200 g to 500 g a.i./ha.

For seed dressing advantageous application rates range from 0.5 g to 1000 g a.i. per 100 kg seed, preferably from 3g to 100 g a.i. per 100kg seed. Most preferred are application rate from 10 g to 50 g a.i. per 100 kg seed.

Suitable carriers and adjuvants can be solid or liquid and correspond to the substances ordinarily employed in formulation technology, e.g. natural or regenerated mineral substances, solvents, dispersants, wetting agents, tackifiers, binders or fertilizers. The formulations, i.e. the entomocidal compositions, preparations or mixtures thereof with other active ingredients, and, where appropriate, a solid or liquid adjuvant, are prepared in known manner, e.g., by homogeneously mixing and/or grinding the active ingredients with extenders, e.g., solvents, solid carriers, and in some cases surface-active compounds (surfactants).

Suitable solvents are: aromatic hydrocarbons, preferably the fractions containing 8 to 12 carbon atoms, e.g. xylene mixtures or substituted naphthalenes, phthalates such as dibutyl phthalate or dioctyl phthalate, aliphatic hydrocarbons such as cyclohexane or paraffins, alcohols and glycols and their ethers and esters, such as ethanol, ethylene glycol monomethyl or monoethyl ether, ketones such as cyclohexanone, strongly polar solvents such as N-methyl-2-pyrrolidone, dimethylsulfoxide or dimethylformamide, as well as vegetable oils or epoxidised vegetable oils such as epoxidised coconut oil or soybean oil; or water.

The solid carriers used, e.g., for dusts and dispersible powders, are normally natural mineral fillers such as calcite, talcum, kaolin, montmorillonite or attapulgite. In order to improve the physical properties it is also possible to add highly dispersed silicic acid or highly dispersed absorbent polymers. Suitable granulated adsorptive carriers are porous types, for example pumice, broken brick, sepiolite or bentonite; and suitable nonsorbent carriers are materials such as calcite or sand. In addition, a great number of pregranulated materials of inorganic or organic nature can be used, e.g. especially dolomite or pulverized plant residues.

Depending on the nature of the active ingredients to be formulated, suitable surface-active compounds are non-ionic, cationic and/or anionic surfactants having good emulsifying, dispersing and wetting properties. The term "surfactants" will also be understood as comprising mixtures of surfactants. Suitable anionic surfactants can be both water-soluble soaps and water-soluble synthetic surface-active compounds. Suitable soaps are the alkali metal salts, alkaline earth metal salts or unsubstituted or substituted ammonium salts of higher fatty acids (C_{sub} 10 - C_{sub} 22), e.g. the sodium or potassium salts of oleic or stearic acid, or of natural fatty acid mixtures which can be obtained, e.g. from coconut oil or tallow oil. Further suitable surfactants are also the fatty acid methyltaurin salts as well as modified and unmodified phospholipids.

More frequently, however, so-called synthetic surfactants are used, especially fatty sulfonates, fatty sulfates, sulfonated benzimidazole derivatives or alkylarylsulfonates. The fatty sulfonates or sulfates are usually in the forms of alkali metal salts, alkaline earth metal salts or unsubstituted or substituted ammonium salts and generally contain a C_{sub} 8 - C_{sub} 22 alkyl radical which also includes the alkyl moiety of acyl radicals, e.g. the sodium or calcium salt of lignosulfonic acid, of dodecylsulfate, or of a mixture of fatty alcohol sulfates obtained from natural fatty acids. These compounds also comprise the salts of sulfuric acid esters and sulfonic acids of fatty alcohol/ethylene oxide adducts. The sulfonated

benzimidazole derivatives preferably contain 2 sulfonic acid groups and one fatty acid radical containing about 8 to 22 carbon atoms. Examples of alkylarylsulfonates are the sodium, calcium or triethanolamine salts of dodecylbenzenesulfonic acid, dibutyl-naphthalenesulfonic acid, or of a naphthalenesulfonic acid/formaldehyde condensation product. Also suitable are corresponding phosphates, e.g. salts of the phosphoric acid ester of an adduct of p-nonylphenol with 4 to 14 moles of ethylene oxide. Non-ionic surfactants are preferably polyglycol ether derivatives of aliphatic or cycloaliphatic alcohols, or saturated or unsaturated fatty acids and alkylphenols, said derivatives containing 3 to 30 glycol ether groups and 8 to 20 carbon atoms in the (aliphatic) hydrocarbon moiety and 6 to 18 carbon atoms in the alkyl moiety of the alkylphenols.

Further suitable non-ionic surfactants are the water-soluble adducts of polyethylene oxide with polypropylene glycol, ethylenediaminopolypropylene glycol and alkylpolypropylene glycol containing 1 to 10 carbon atoms in the alkyl chain, which adducts contain 20 to 250 ethylene glycol ether groups and 10 to 100 propylene glycol ether groups. These compounds usually contain 1 to 5 ethylene glycol units per propylene glycol unit. Representative examples of non-ionic surfactants are nonylphenolpolyethoxyethanols, castor oil polyglycol ethers, polypropylene/polyethylene oxide adducts, tributylphenoxypolyethoxyethanol, polyethylene glycol and octylphenoxypolyethoxyethanol. Fatty acid esters of polyoxyethylene sorbitan, such as polyoxyethylene sorbitan trioleate, are also suitable non-ionic surfactants.

Cationic surfactants are preferably quaternary ammonium salts which contain, as N-substituent, at least one C₈-C₂₂ alkyl radical and, as further substituents, lower unsubstituted or halogenated alkyl, benzyl or hydroxyl-lower alkyl radicals. The salts are preferably in the form of halides, methylsulfates or ethylsulfates, e.g., stearyltrimethylammonium chloride or benzyldi-(2-chloroethyl)ethylammonium bromide.

The surfactants customarily employed in the art of formulation are described, e.g., in "McCutcheon's Detergents and Emulsifiers Annual", MC Publishing Corp. Ridgewood, N.J., 1979; Dr. Helmut Stache, "Tensid Taschenbuch" (Handbook of Surfactants), Carl Hanser Verlag, Munich/Vienna.

Another particularly preferred characteristic of an entomocidal composition of the present invention is the persistence of the active ingredient when applied to plants and soil. Possible causes for loss of activity include inactivation by ultra-violet light, heat, leaf exudates and pH. For example, at high pH, particularly in the presence of reductant, δ -endotoxin crystals are solubilized and thus become more accessible to proteolytic

inactivation. High leaf pH might also be important, particularly where the leaf surface can be in the range of pH 8-10. Formulation of an entomocidal composition to be used in a method according to the present invention can address these problems by either including additives to help prevent loss of the active ingredient or encapsulating the material in such a way that the active ingredient is protected from inactivation. Encapsulation can be accomplished chemically (McGuire and Shasha, J Econ Entomol 85: 1425-1433, 1992) or biologically (Barnes and Cummings, 1986; EP-A 0 192 319). Chemical encapsulation involves a process in which the active ingredient is coated with a polymer while biological encapsulation involves the expression of the δ -endotoxin genes in a microbe. For biological encapsulation, the intact microbe containing the toxin protein is used as the active ingredient in the formulation. The addition of UV protectants might effectively reduce irradiation damage. Inactivation due to heat could also be controlled by including an appropriate additive.

Preferred within the present application are formulations comprising living microorganisms as an active ingredient either in form of the vegetative cell or more preferable in form of spores, if available. Suitable formulations may consist, for example, of polymer gels which are crosslinked with polyvalent cations and comprise these microorganisms. This is described, for example, by D.R. Fravel et al. in *Phytopathology*, Vol. 75, No. 7, 774-777, 1985 for alginate as the polymer material. It is also known from this publication that carrier materials can be co-used. These formulations are as a rule prepared by mixing solutions of naturally occurring or synthetic gel-forming polymers, for example alginates, and aqueous salt solutions of polyvalent metal ions such that individual droplets form, it being possible for the microorganisms to be suspended in one of the two or in both reaction solutions. Gel formation starts with the mixing in drop form. Subsequent drying of these gel particles is possible. This process is called ionotropic gelling. Depending on the degree of drying, compact and hard particles of polymers which are structurally crosslinked via polyvalent cations and comprise the microorganisms and a carrier present predominantly uniformly distributed are formed. The size of the particles can be up to 5 mm.

Compositions based on partly crosslinked polysaccharides which, in addition to a microorganism, for example, can also comprise finely divided silicic acid as the carrier material, crosslinking taking place, for example, via Ca^{++} ions, are described in EP-A1-0 097 571. The compositions have a water activity of not more than 0.3. W.J. Cornick et al. describe in a review article [New Directions in Biological Control: Alternatives for Suppressing Agricultural Pests and Diseases, pages 345-372, Alan R. Liss, Inc. (1990)]

various formulation systems, granules with vermiculite as the carrier and compact alginate beads prepared by the ionotropic gelling process being mentioned. Such compositions are also disclosed by D.R.Fravel in Pesticide Formulations and Application Systems: 11th Volume, ASTM STP 1112 American Society for Testing and Materials, Philadelphia, 1992, pages 173 to 179 and can be used to formulate the recombinant microorganisms according to the invention. Further methods for formulating living microorganism are described in WO96/02638.

The compositions according to the invention are valuable for preventive and/or curative treatment in the field of pest control even at low rates of application while being well tolerated by and non-toxic to warm-blooded species, fish and plants and have a very favourable biocidal spectrum. The compositions according to the invention are active against all or individual development stages of *Ostrinia furnacalis* (*Asian Corn Borer*) pests. The insecticidal action of the compounds according to the invention can become obvious either directly, i.e. by destroying the pests immediately or only after some time has elapsed.

The said composition can be provided in form of a chemical mixture comprising the toxin proteins in an essentially pure form or in form of a mixture comprising at least one of the toxin proteins as part of a microorganism or a transgenic plant.

In a specific embodiment of the invention, one of the active ingredients may be applied to the plant directly by, for example, leaf application as described herein previously, whereas the second active principle may be provided by the plant itself upon expression of a previously transformed gene encoding the said second principle.

The entomocidal compositions to be used in the method according to the invention usually contain from about 0.1 to about 99%, preferably from about 0.1 to about 95%, and most preferably from about 3 to about 90% of active ingredient; from about 1 to about 99.9%, preferably from about 1 to about 99%, and most preferably from about 5 to about 95% of a solid or liquid adjuvant; and from about 0 to about 25%, preferably about 0.1 to about 25%, and most preferably from about 0.1 to about 20% of a surfactant.

Whereas commercial products are preferably formulated as concentrates, the end user will normally employ dilute formulations of substantially lower concentration. The entomocidal compositions may also contain further ingredients, such as stabilizers,

antifoams, viscosity regulators, binders, tackifiers as well as fertilizers or other active ingredients in order to obtain special effects.

The present invention also relates to formulations comprising living microorganisms as an active ingredient which are present in the form of vegetative cells or more in the form of spores, if available.

A further object of the invention relates to the use of recombinant microorganisms comprising a toxin gene encoding a toxin protein of *Bacillus thuringiensis* such as a CryI-type protein, in a method of controlling crop plants against damages caused by *Ostrinia furnacalis* (*Asian Corn Borer*) species, which recombinant organisms are either applied directly to the plant to be protected or the recombinantly produced toxin protein is first isolated from the recombinant microorganism and formulated as described above before being applied to the crop plant to be protected. The recombinant microorganisms may also contain a toxin gene encoding a VIP-type toxin protein as disclosed in the EP-A-690 916 and the International Application No EP95/03826 or a combination of genes encoding at least a Cry-type toxin and a VIP-type toxin, respectively.

For recombinant production of the toxin protein in a host organism, the coding sequence may be inserted into an expression cassette designed for the chosen host and introduced into the host where it is recombinantly produced. The choice of specific regulatory sequences such as promoter, signal sequence, 5' and 3' untranslated sequences, and enhancer appropriate for the chosen host is within the level of skill of the practitioner in the art. The resultant molecule, containing the individual elements linked in the proper reading frame, are inserted into a vector capable of being transformed into the host cell. Suitable expression vectors and methods for recombinant production of proteins are well known for host organisms such as *E. coli* (see, e.g. Studier and Moffatt, *J. Mol. Biol.* 189: 113 (1986); Brosius, *DNA* 8: 759 (1989)), yeast (see, e.g., Schneider and Guarente, *Meth. Enzymol.* 194: 373 (1991)) and insect cells (see, e.g., Luckow and Summers, *Bio/Technol.* 6: 47 (1988)). Specific examples include plasmids such as pBluescript (Stratagene, La Jolla, CA), pFLAG (International Biotechnologies, Inc., New Haven, CT), pTrcHis (Invitrogen, La Jolla, CA), and baculovirus expression vectors, e.g., those derived from the genome of *Autographica californica* nuclear polyhedrosis virus

(AcMNPV). A preferred baculovirus/insect system is pVI11392/Sf21 cells (Invitrogen, La Jolla, CA).

The recombinantly produced toxin protein can be isolated and purified using a variety of standard techniques. The actual techniques which may be used will vary depending upon the host organism used, whether the toxin protein is designed for secretion, and other such factors a skilled artisan is aware of (*see, e.g.* chapter 16 of Ausubel, F. *et al.*, "Current Protocols in Molecular Biology", pub. by John Wiley & Sons, Inc. (1994)).

A preferred object of the invention relates to the use of transgenic plants comprising and expressing a toxin gene encoding a toxin protein of *Bacillus thuringiensis*, especially a CryI-type toxin protein, in an amount sufficient to provide control against *Ostrinia furnacalis* (*Asian Corn Borer*) species, in a method of protecting crop plants against damages caused by *Ostrinia furnacalis* (*Asian Corn Borer*) pests. The plants can be the result of nuclear transformation or plastid transformation (see WO 95/24492). Especially preferred are transgenic plants expressing a CryIA(b) toxin protein of *Bacillus thuringiensis*. The invention also relates to the use of transgenic plants comprising a toxin gene encoding a VIP-type protein as described in EP-A-690 916 and International Application No EP95/03826, herein incorporated by reference in its entirety. The invention also relates to the use of transgenic plants comprising and expressing a toxin gene encoding a toxin protein of *Bacillus thuringiensis*, but especially a Cry-type toxin protein, and also comprising and expressing a toxin gene encoding a VIP-type protein in an amount sufficient to provide control against *Ostrinia furnacalis* (*Asian Corn Borer*) species. A host plant expressing said toxin genes will have enhanced resistance to insect attack of *Ostrinia furnacalis* (*Asian Corn Borer*) species and will be better equipped to withstand crop losses associated with such attack.

In one preferred embodiment, expression of one or more Bt δ -endotoxins in a transgenic plant is accompanied by the expression of one or more VIP-type proteins. This co-expression of more than one insecticidal principle in the same transgenic plant can be achieved by genetically engineering a plant to contain and express all the genes necessary. Alternatively, a plant, Parent 1, can be genetically engineered for the expression of VIP-type proteins. A second plant, Parent 2, can be genetically engineered for the expression of Bt δ -endotoxin. By crossing Parent 1 with Parent 2, progeny plants are obtained which

express all the genes introduced into Parents 1 and 2. Particularly preferred Bt δ -endotoxins are those disclosed in EP-A 0618976, herein incorporated by reference.

Also comprised by the present invention is the use of recombinant microorganisms or transgenic plants comprising a gene encoding DNA molecules which hybridizes to a DNA molecule encoding a toxin protein of *Bacillus* species, but preferably to an oligonucleotide probe obtainable from said DNA molecule comprising a contiguous portion of the coding sequence for the said toxin protein at least 10 nucleotides in length, under moderately stringent conditions. The invention preferably comprises the use of recombinant microorganisms or transgenic plants comprising a gene encoding DNA molecules which hybridizes to a DNA molecule encoding a toxin protein of *Bacillus thuringiensis* or *B cereus* especially to a DNA molecule encoding a Cry-type protein or to a toxin gene encoding a VIP-type toxin protein, preferably to a CryIA(b) protein.

Factors that effect the stability of hybrids determine the stringency of the hybridization. One such factor is the melting temperature T_m which can be easily calculated according to the formula provided in DNA PROBES, George H. Keller and Mark M. Manak, Macmillan Publishers Ltd, 1993, Section one: Molecular Hybridization Technology; page 8 ff.

The preferred hybridization temperature is in the range of about 25°C below the calculated melting temperature T_m and preferably in the range of about 12-15°C below the calculated melting temperature T_m and in the case of oligonucleotides in the range of about 5-10°C below the melting temperature T_m .

The invention further relates to a commercial bag comprising seed of a transgenic plant comprising at least a toxin gene encoding a toxin protein of *Bacillus thuringiensis*, preferably a Cry-type toxin protein, more preferably a CryI-type toxin protein, but most preferably a CryIA-type toxin protein and expressing the said toxin protein in an amount sufficient to provide control against *Ostrinia furnacalis* (*Asian Corn Borer*) species, together with label instructions for the use thereof for control of *Ostrinia furnacalis* (*Asian Corn Borer*) pests in crop plants. Preferred within this invention is a commercial bag comprising seed of a transgenic plant comprising as an active ingredient a gene encoding at least a Cry-type

toxin protein and a VIP-type protein. Especially preferred is a combination of a CryIA(b) toxin protein with a VIP-type protein.

The further object of the invention is a commercial bag comprising an insecticidal composition according to the invention together with label instructions for the use thereof for control of *Ostrinia furnacalis* (*Asian Corn Borer*) pests in crop plants.

By plant is meant any plant species which can be genetically transformed by methods known in the art, but especially those plants that are host plants for *Ostrinia furnacalis* (*Asian Corn Borer*) species including, but not limited to, the following species of plants: maize, wheat, barley, rye, oats, rice, sorghum, millet and related crops, forage grasses, bamboo (orchardgrass, fescue, and the like), and sugar cane.

Methods known in the art for plant transformation are discussed below. Host plants include, but are not limited to, those species previously listed as target crops.

The invention further relates to seed of a transgenic plant comprising a gene encoding a toxin protein of *Bacillus thuringiensis* and expressing said toxin protein in an amount sufficient to provide control against *Ostrinia furnacalis* (*Asian Corn Borer*) species, and a commercial bag containing said seed.

By plant is meant any plant species that is a host for *Ostrinia furnacalis* (*Asian Corn Borer*) including, but not limited to, the species of maize, wheat, barley, rye, oats, rice, sorghum, millet and related crops, forage grasses, bamboo and sugar cane.

It has been discovered that the codon usage of a native *Bacillus thuringiensis* toxin gene is significantly different from that which is typical of a plant gene. In particular, the codon usage of a native *Bacillus thuringiensis* gene is very different from that of a maize gene. As a result, the mRNA from this gene may not be efficiently utilized. Codon usage might influence the expression of genes at the level of translation or transcription or mRNA processing. To optimize a toxin gene for expression in plants, for example in maize, the codon usage is optimized by using the codons which are most preferred in maize (maize preferred codons) in the synthesis of a synthetic gene which encodes the same protein as found for the native toxin gene sequence. The optimized maize preferred codon usage is effective for expression of high levels of the *Bt* insecticidal

protein. Further details for constructing maize-optimized synthetic toxin genes can be found in WO 93/07278, herein incorporated by reference in its entirety.

Toxin genes derived from microorganisms may also differ from plant genes. Plant genes differ from genes found in microorganisms in that their transcribed RNA does not possess defined ribosome binding site sequence adjacent to the initiating methionine. Consequently, microbial genes can be enhanced by the inclusion of a eukaryotic consensus translation initiator at the ATG. Clontech (1993/1994 catalog, page 210) has suggested the sequence GTCGACCATGGTC as a consensus translation initiator for the expression of the *E. coli uidA* gene in plants. Further, Joshi (Nucl Acids Res 15: 6643-6653 (1987)) has compared many plant sequences adjacent to the ATG and suggests the consensus TAAACAATGGCT. In situations where difficulties are encountered in the expression of microbial ORFs in plants, inclusion of one of these sequences at the initiating ATG may improve translation. In such cases the last three nucleotides of the consensus may not be appropriate for inclusion in the modified sequence due to their modification of the second amino acid residue. Preferred sequences adjacent to the initiating methionine may differ between different plant species. By surveying the sequence of maize genes present in the GenBank/EMBL database it can be discerned which nucleotides adjacent to the ATG should be modified to enhance translation of the toxin gene introduced into maize.

In addition, it has been shown that removal of illegitimate splice sites can enhance expression and stability of introduced genes. Genes cloned from non-plant sources and not optimized for expression in plants may contain motifs which can be recognized in plants as 5' or 3' splice sites. Consequently, the transcription process can be prematurely terminated, generating truncated or deleted mRNA. The toxin genes can be engineered to remove these illegitimate splice sites using techniques well known in the art.

Many δ -endotoxin proteins from *Bacillus thuringiensis* are expressed as protoxins. These protoxins are solubilized in the alkaline environment of the insect gut and are then proteolytically converted by proteases into a toxic core fragment (Höfte and Whiteley, Microbiol. Rev. 53: 242-255 (1989)). For δ -endotoxin proteins of the CryI class, the toxic core fragment is localized in the N-terminal half of the protoxin. It is within the scope of the present invention that genes encoding either the full-length protoxin form or the

truncated toxic core fragment of the novel toxin protein can be used in plant transformation vectors to confer insecticidal properties upon the host plant.

The recombinant DNA molecules can be introduced into the plant cell in a number of art-recognized ways. Those skilled in the art will appreciate that the choice of method might depend on the type of plant, i.e. monocot or dicot, targeted for transformation. Suitable methods of transforming plant cells include microinjection (Crossway et al., *BioTechniques* 4:320-334 (1986)), electroporation (Riggs et al, *Proc. Natl. Acad. Sci. USA* 83:5602-5606 (1986)), *Agrobacterium*-mediated transformation (Hinchey et al., *Biotechnology* 6:915-921 (1988)), direct gene transfer (Paszkowski et al., *EMBO J.* 3:2717-2722 (1984)), and ballistic particle acceleration using devices available from Agracetus, Inc., Madison, Wisconsin and Dupont, Inc., Wilmington, Delaware (see, for example, Sanford et al., U.S. Patent 4,945,050; and McCabe et al., *Biotechnology* 6:923-926 (1988)). See also, Weissinger et al., *Annual Rev. Genet.* 22:421-477 (1988); Sanford et al., *Particulate Science and Technology* 5:27-37 (1987)(onion); Christou et al., *Plant Physiol.* 87:671-674 (1988)(soybean); McCabe et al., *Bio/Technology* 6:923-926 (1988)(soybean); Datta et al., *Bio/Technology* 8:736-740 (1990)(rice); Klein et al., *Proc. Natl. Acad. Sci. USA*, 85:4305-4309 (1988)(maize); Klein et al., *Bio/Technology* 6:559-563 (1988)(maize); Klein et al., *Plant Physiol.* 91:440-444 (1988)(maize); Fromm et al., *Bio/Technology* 8:833-839 (1990); and Gordon-Kamm et al., *Plant Cell* 2:603-618 (1990)(maize); Svab et al. *Proc. Natl. Acad. Sci. USA* 87: 8526-8530 (1990) (tobacco chloroplast); Koziel *et al.* (*Biotechnology* 11: 194-200 (1993)) (maize); Shimamoto *et al.* *Nature* 338: 274-277 (1989) (rice); Christou *et al.* *Biotechnology* 9: 957-962 (1991) (rice); European Patent Application EP 0 332 581 (orchardgrass and other *Pooideae*); Vasil *et al.* (*Biotechnology* 11: 1553-1558 (1993) (wheat); Weeks *et al.* (*Plant Physiol.* 102: 1077-1084 (1993) (wheat); Wan *et al.* (*Plant Physiol.* 104: 37-48 (1994) (barley); Umbeck *et al.* (*Bio/Technology* 5: 263-266 (1987) (cotton).

One particularly preferred set of embodiments for the introduction of recombinant DNA molecules into maize by microprojectile bombardment can be found in WO 93/07278, herein incorporated by reference in its entirety. An additional preferred embodiment is the protoplast transformation method for maize as disclosed in Application EP-A-292 435, hereby incorporated by reference in its entirety.

The genetic properties engineered into the transgenic seeds and plants described above are passed on by sexual reproduction or vegetative growth and can thus be

maintained and propagated in progeny plants. Generally said maintenance and propagation make use of known agricultural methods developed to fit specific purposes such as tilling, sowing or harvesting. Specialized processes such as hydroponics or greenhouse technologies can also be applied. As the growing crop is vulnerable to attack and damages caused by insects or infections as well as to competition by weed plants, measures are undertaken to control weeds, plant diseases, insects, nematodes, and other adverse conditions to improve yield. These include mechanical measures such as tillage of the soil or removal of weeds and infected plants, as well as the application of agrochemicals such as herbicides, fungicides, gametocides, nematocides, growth regulants, ripening agents and insecticides.

Use of the advantageous genetic properties of the transgenic plants and seeds according to the invention can further be made in plant breeding which aims at the development of plants with improved properties such as tolerance of pests, herbicides, or stress, improved nutritional value, increased yield, or improved structure causing less loss from lodging or shattering. The various breeding steps are characterized by well-defined human intervention such as selecting the lines to be crossed, directing pollination of the parental lines, or selecting appropriate progeny plants. Depending on the desired properties different breeding measures are taken. The relevant techniques are well known in the art and include but are not limited to hybridization, inbreeding, backcross breeding, multiline breeding, variety blend, interspecific hybridization, aneuploid techniques, etc. Hybridization techniques also include the sterilization of plants to yield male or female sterile plants by mechanical, chemical or biochemical means. Cross pollination of a male sterile plant with pollen of a different line assures that the genome of the male sterile but female fertile plant will uniformly obtain properties of both parental lines. Thus, the transgenic seeds and plants according to the invention can be used for the breeding of improved plant lines which for example increase the effectiveness of conventional methods such as herbicide or pesticide treatment or allow to dispense with said methods due to their modified genetic properties. Alternatively new crops with improved stress tolerance can be obtained which, due to their optimized genetic "equipment", yield harvested product of better quality than products which were not able to tolerate comparable adverse developmental conditions.

In seeds production germination quality and uniformity of seeds are essential product characteristics, whereas germination quality and uniformity of seeds harvested and sold by

the farmer is not important. As it is difficult to keep a crop free from other crop and weed seeds, to control seedborne diseases, and to produce seed with good germination, fairly extensive and well-defined seed production practices have been developed by seed producers, who are experienced in the art of growing, conditioning and marketing of pure seed. Thus, it is common practice for the farmer to buy certified seed meeting specific quality standards instead of using seed harvested from his own crop. Propagation material to be used as seeds is customarily treated with a protectant coating comprising herbicides, insecticides, fungicides, bactericides, nematocides, molluscicides or mixtures thereof. Customarily used protectant coatings comprise compounds such as captan, carboxin, thiram (TMTD[®]), methalaxyl (Apron[®]), and pirimiphos-methyl (Actellic[®]). If desired these compounds are formulated together with further carriers, surfactants or application-promoting adjuvants customarily employed in the art of formulation to provide protection against damage caused by bacterial, fungal or animal pests. The protectant coatings may be applied by impregnating propagation material with a liquid formulation or by coating with a combined wet or dry formulation. Other methods of application are also possible such as treatment directed at the buds or the fruit.

It is a further aspect of the present invention to provide new agricultural methods such as the methods exemplified above which are characterized by the use of transgenic plants, transgenic plant material, or transgenic seed according to the present invention to provide control against *Ostrinia furnacalis* (*Asian Corn Borer*).

To breed progeny from plants transformed according to the method of the present invention, a method such as that which follows may be used: maize plants produced as described in the examples set forth below are grown in pots in a greenhouse or in soil, as is known in the art, and permitted to flower. Pollen is obtained from the mature tassel and used to pollinate the ears of the same plant, sibling plants, or any desirable maize plant. Similarly, the ear developing on the transformed plant may be pollinated by pollen obtained from the same plant, sibling plants, or any desirable maize plant. Transformed progeny obtained by this method may be distinguished from non-transformed progeny by the presence of the introduced gene(s) and/or accompanying DNA (genotype), or the phenotype conferred. The transformed progeny may similarly be selfed or crossed to other plants, as is normally done with any plant carrying a desirable trait. Similarly, tobacco or other transformed plants produced by this method may be selfed or crossed as is known in

the art in order to produce progeny with desired characteristics. Similarly, other transgenic organisms produced by a combination of the methods known in the art and this invention may be bred as is known in the art in order to produce progeny with desired characteristics.

EXAMPLES

The following examples further describe materials and methods used to obtain specific embodiments of the present invention. They are offered by way of illustration, and should not be interpreted as limiting the disclosure of the specification.

EXAMPLE 1: General Methods

DNA manipulations were done using procedures that are routinely practiced in the art. These procedures can often be modified and/or substituted without substantively changing the result. Except where other references are identified, the procedures are described in general text books such as Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, second edition, 1989.

EXAMPLE 2: Plant Transformation Vectors

Plant transformation is accomplished using the transformation vectors pCIB 4431 and pCIB 3064 described in WO 93/07278 and Koziel *et al* (1993) [Biotechnology Vol 11, 194-200], both disclosures being incorporated herein by reference.

pCIB4431 is a vector designed to transform maize. It contains two chimeric synthetic *Bt cryIA(b)* endotoxin genes expressible in maize the one of them constituting a PEP carboxylase promoter/synthetic-*cryIA(b)* gene, the other one a pollen promoter/synthetic-*cryIA(b)* gene.

pCIB4431 contains the synthetic *cryIA(b)* gene provided in SEQ ID NO: 1 and was deposited on September 21, 1992 with the Agricultural Research Service, Patent Culture Collection (NRRL), Northern Regional Research Center, 1815 North University Street, Peoria, Illinois 61604, U.S.A. under accession no NRRL B-18998.

pCIB3064 contains a plant expressible *bar* gene (615 bp), which was originally cloned from *Streptomyces hygrosopicus* [Thompson *et al.* (1987) EMBO J 6, 2519-2523]. It encodes a phosphinotricin acetyltransferase (PAT), conferring tolerance to phosphinotricin. The *bar* gene is under the control of the CaMV 35S promoter and terminator [OW *et al* (1987) Proc Natl Acad Sci USA 84, 4870-4874] to provide resistance to phosphinotricin.

EXAMPLE 3: Production of transgenic maize plants containing the synthetic maize CryIA(b) gene

The example below utilizes a biolistic device to introduce DNA coated particles into maize cells, from which transformed plants are generated.

3.1 Tissue

Immature maize embryos, approximately 1.5-2.5 mm in length, were excised from an ear of genotype 6N615 14-15 days after pollination. The mother plant was grown in the greenhouse. Before excision, the ear was surface sterilized with 20% Clorox for 20 minutes and rinsed 3 times with sterile water. Individual embryos were plated scutellum side up in a 2 cm square area, 36 embryos to a plate, on the callus initiation medium, 2DG4 + 5 chloramben medium (N6 major salts, B5 minor salts, MS iron, 2% sucrose, with 5 mg/l chloramben, 20 mg/l glucose, and 10 ml G4 additions (Table 1) added after autoclaving.

Table 1: G4 Additions

<u>Ingredient</u>	<u>per liter medium</u>
Casein hydrolysate	0.5 g
Proline	1.38 g
Nicotinic acid	0.2 mg
Pyridoxine-HCl	0.2 mg
Thiamine-HCl	0.5 mg
Choline-HCl	0.1 mg
Riboflavin	0.05 mg
Biotin	0.1 mg
Folic acid	0.05 mg
Ca pantothenate	0.1 mg
p-aminobenzoic acid	0.05 mg
B12	0.136 µg

3.2 Preparation of DNA for delivery

The microcarrier was prepared essentially according to the instructions supplied with the Biolistic device. While vortexing 50 μ l 1.0 μ m gold microcarrier, 5 μ l of pCIB4431 (1.23 μ g/ μ l) [#898] + 2 μ l pCIB3064 (0.895 μ g/ μ l) [#456] was added followed by 50 μ l 2.5 M CaCl_2 , then 20 μ l 0.1 M spermidine (free base, TC grade). The resulting mixture was vortexed 3 minutes and microfuged for 10 sec. The supernatant was removed and the microcarriers washed 2 times with 250 μ l of 100% EtOH (HPLC grade) by vortexing briefly, centrifuging and removing the supernatant. The microcarriers are resuspended in 65 μ l 100% EtOH.

3.3 Bombardment

Tissue was bombarded using the PDS-1000He Biolistics device. The tissue was placed on the shelf 8 cm below the stopping screen shelf. The tissue was shot one time with the DNA/gold microcarrier solution, 10 μ l dried onto the macrocarrier. The stopping screen used was hand punched using 10x10 stainless steel mesh screen. Rupture discs of 1550 psi value were used. After bombardment, the embryos were cultured in the dark at 25° C.

3.4 Callus formation

Embryos were transferred to callus initiation medium with 3 mg/l PPT 1 day after bombardment. Embryos were scored for callus initiation at 2 and 3 weeks after bombardment. Any responses were transferred to callus maintenance medium, 2DG4 + 0.5 2,4-D medium with 3 mg/L PPT. Callus maintenance medium is N6 major salts, B5 minor salts, MS iron, 2% sucrose, with 0.5 mg/l 2,4-D, 20 mg/l glucose, and 10 ml G4 additions added after autoclaving. Embryogenic callus was subcultured every 2 weeks to fresh maintenance medium containing 3 mg/L PPT. All callus was incubated in the dark at 25°C.

The Type I callus formation response was 15%. Every embryo which produced callus was cultured as an individual event giving rise to an individual line.

3.5 Regeneration

After 12 weeks on selection, the tissue was removed from callus maintenance medium with PPT and was placed on regeneration medium. Regeneration medium is 0.25MS3S5BA (0.25 mg/l 2,4 D, 5 mg/l BAP, MS salts, 3% sucrose) for 2 weeks followed by subculture to MS3S medium for regeneration of plants. After 4 to 10 weeks, plants were removed and put into GA 7's.

EXAMPLE 4: Analysis of transgenic maize plants

4.1 ELISA Assay

Detection of cryIA(b) gene expression in transgenic maize is monitored using Asian corn borer insect bioassays and ELISA analysis for a quantitative determination of the level of cryIA(b) protein obtained.

Quantitative determination of cryIA(b) insecticidal protein in the leaves of transgenic plants is performed using enzyme-linked immunosorbent assays (ELISA) as disclosed in Clark M F, Lister R M, Bar-Joseph M: ELISA Techniques. In: Weissbach A, Weissbach H (eds) Methods in Enzymology 118:742-766, Academic Press, Florida (1986). Immunoaffinity purified polyclonal rabbit and goat antibodies specific for the B. thuringiensis subsp. kurstaki insecticidal protein are used to determine the amount of insecticidal protein per mg soluble protein from crude extracts of leaf samples. The sensitivity of the double sandwich ELISA is 1-5 ng insecticidal protein per mg soluble protein using 50 µg of total protein per ELISA microtiter dish well.

Corn extracts are made by grinding leaf tissue in gauze lined plastic bags using a hand held ball-bearing homogenizer (AGDIA, Elkart IN.) in the presence of extraction buffer (50 mM Na₂CO₃ pH 9.5, 100 mM NaCl, 0.05% Triton, 0.05% Tween, 1 mM PMSF and 1 µM leupeptin). Protein determination is performed using the Bio-Rad (Richmond, CA) protein assay.

4.2 Asian Corn Borer Assay

One to four 4 cm sections are cut from an extended leaf of a corn plant. Each leaf piece is placed on a moistened filter disc in a 50 x 9 mm petri dish. Five neonate Asian corn borer larvae are placed on each leaf piece (making a total of 5-20 larvae per plant). The petri

dishes are incubated at 29.5 °C. Leaf feeding damage and mortality data are scored after 24, 48, and 72 hours.

EXAMPLE 5: *Ostrinia furnacalis* (Asian Corn Borer) Field Testing Assay

Small peat pots containing transgenic seedlings which were first tested for the presence and the expression of the transgene, are transplanted into the field. Non-transgenic inbred lines are planted in the same field over a six week period, to serve as controls and for pollinations.

When plants in the field reach 40 cm of extended leaf height, infestation with laboratory-reared *Ostrinia furnacalis* (Asian Corn Borer) larvae begins on both the transgenic and non-transgenic control plants. About 300 neonate larvae mixed with corn cob grits are introduced into the whorl of each plant using a Davis inoculator. Infestations continues on a weekly basis for four weeks to stimulate first generation Asian Corn Borer. Starting two weeks after the initial infestation, each plant is rated weekly for four weeks using a 1 to 9 scale (1= no visible leaf injury; 9=most leaf with long lesions, several leaves with broken mid ribe, possibly stunted plants due to Asian Corn Borer feeding). A mean Asian Corn Borer damage rating score is calculated for each transgenic and non-transgenic control plant. As each plant reaches anthesis, 300 larvae/plant are applied weekly for four weeks to stimulate second generation infestation. One hundred of neonate larvae in corn cob grits are introduced into the leaf axil at the primary ear and at the leaf axil one node above and below the primary ear node. Therefore a total of approximatively 2400 larvae are applied to each plant. About 50 days after the initial second generation infestation, stalks from all transplanted and some non-transgenic plants are harvested. The extent of internal second generation infestation tunneling damage in the whole plants is determined.

EXAMPLE 6: Assay of extract from transformed protoplasts for insecticidal activity against *Ostrinia furnacalis* (Asian Corn Borer)

Western blot analysis is performed using extracts obtained from maize cells which had been transiently transformed with DNA to express the maize optimized gene.

Qualitative insect toxicity testing is carried out using harvested protoplasts. Suspensions are prepared for each replicate tested in the bioassays. A replicate is considered positive if it causes significantly higher mortality than the controls. For example, replicates are tested for their activity against insects in the order Lepidoptera by using the Asian corn borer,

Ostrinia furnacalis. One-hundred µl of a protoplast suspension in 0.1% Triton X-100 is pipetted onto the surface of artificial Black cutworm diet, (Bioserv, Inc., Frenchtown, NJ; F9240) in 50 mm x 10 mm snap-cap petri dishes. After air drying 10 neonatal larvae are added to each plate. Mortality is recorded after about 4 days.

EXAMPLE 7: *Ostrinia furnacalis* (Asian Corn Borer) Plant Dipping Assay

7.1 *Bacillus thuringiensis* (Bt) crystals

Bacillus thuringiensis (Bt) crystals are prepared for stock suspension with 22 ml of distilled water. The suspension is kept in the refrigerator.

7.2 Parameters recorded

3 days old larvae of *Ostrinia furnacalis* (*Asian Corn Borer*) are allowed to feed on maize leaves. Larvae had previously been fed with untreated leaves. 120 hours later the number of larvae dead is recorded. The kind of feeding injuries on leaf plants is observed in each case.

7.3 Method for testing

Plants of two homozygous inbred lines of *Zea mays* susceptible to Asian Corn Borer are used (Lines A and B). Seedling plants aged 9-10 days are dipped in various concentrations of Bt protein suspension and are used in feeding experiments, wherein larvae are released on dried leaves of seedling plants, 5-10 larvae per plant. The seedling plants are covered with nylon mesh bags and kept in a nylon mesh case. 4-5 concentrations with 4 replications are tested and mortality is determined. The temperature is kept at 21-30°C.

7.4 Results**Table 2:** Results for Line A

Dose [ppm]	Number of insects	Number of dead insects	Mortality [%]
80	40	31	77.5
40	40	29	72.5
20	40	15	37.5
10	40	13	32.5
5	40	5	12.5
0	40	0	0.00

Table 3: Results for Line B

Dose [ppm]	Number of insects	Number of dead insects	Mortality [%]
80	40	38	94.74
40	40	33	81.58
20	40	28	68.42
10	40	19	44.74
5	40	10	21.05
0	40	2	5.00

Two kinds of injuries were clearly distinguished in maize leaves: Bt dipped leaves of the seedling plants were lightly damaged, whereas the leaves of control seedlings were severely damaged.

The following LC_{50} -Values were obtained:

Line A: $LC_{50} = 23.412$ ppm (range from 17.834 to 30.734)

Line B: $LC_{50} = 12.234$ ppm (range from 9.547 to 15.676)

EXAMPLE 8: *Ostrinia furnacalis* (Asian Corn Borer) Plant Dipping Assay (VIP3A)

8.1 VIP3A protein

5mg of VIP3A protein were prepared with 50ml of distilled water in order to prepare varying concentration of VIP3 protein: 100ppm, 50ppm, 25ppm, 12.5ppm, 6.25ppm and 0ppm (check).

8.2 *Ostrinia furnacalis* (Asian Corn Borer)

The pupae collected from farmers field at Racha Buri by Entomology and Animal Science Division DOA is order to prepare Larvae (L2) for testing.

8.3 Parameters recorded

Data were collected after incubation 5 days by counting number of died larvae and then analyzed percentage of mortality of larvae by probit Analysis Program.

7.3 Method for testing

Plants of two homozygous inbred lines of *Zea mays* susceptible to Asian Corn Borer are used (Lines B and C). Line B was conducted for potted plant test (4 replications 5 rated concentration and check) and Line C was conducted for leaf dipping test (4 replications with 100, 50, 25ppm and check). Seedling plants aged 10-14 days are dipped in various concentrations of VIP3A protein suspension and are used in feeding experiments, wherein larvae are released on dried leaves of seedling plants, 5-10 larvae per plant. The seedling plants are covered with nylon mesh bags and kept in a nylon mesh case. Cut leaves were put in plastic blocks and kept in control room four replications were applied for this experiment.

7.4 Results

Table 4: Results for Line B**Table 4a**

Dose [ppm]	Number of insects	Number of dead insects	Mortality [%]
100	40	31	76.92
50	40	26	64.10
25	40	16	38.46
12.5	40	14	33.33
6.25	40	9	20.51
0	40	1	2.50

Table 4b

Replication	number of dead larvae after 5 days					
	concentration (ppm)					
	Check	6.25	12.5	25	50	100
I (10)	0	3	3	5	8	6
II (10)	0	2	2	3	6	9
III (10)	1	3	5	4	5	9
IV (10)	0	1	4	4	7	7
Total	1	9	14	16	26	31

Table 5: Results for Line C**Table 5a**

Replication	number of dead larvae after 24 hours			
	concentration (ppm)			
	Check	25	50	100
I (10)	0	0	0	1
II (10)	0	0	0	1
III (10)	0	0	0	0
IV (10)	0	0	0	1
Total	0	0	0	3

Table 5b

Replication	number of dead larvae after 48 hours			
	concentration (ppm)			
	Check	25	50	100
I (10)	0	0	0	1
II (10)	0	0	0	1
III (10)	0	0	1	0
IV (10)	0	0	0	1
Total	0	0	1	3

Table 5c

Replication	number of dead larvae after 72 hours			
	concentration (ppm)			
	Check	25	50	100
I (10)	0	1	0	2
II (10)	0	1	0	1
III (10)	0	0	2	3
IV (10)	0	0	2	1
Total	0	2	4	7

Table 5d

Replication	number of dead larvae after 96 hours			
	concentration (ppm)			
	Check	25	50	100
I (10)	0	1	1	4
II (10)	0	2	1	3
III (10)	0	1	3	5
IV (10)	0	1	4	3
Total	0	5	1	15

Table 5e

Replication	number of dead larvae after 120 hours			
	concentration (ppm)			
	Check	25	50	100
I (10)	1	3	2	7
II (10)	0	2	1	4
III (10)	0	3	5	5
IV (10)	0	2	4	9
Total	1	10	12	25

The following LC_{50} -Values were obtained after 120 hours

Line B: $LC_{50} = 29.558$ ppm (range from 21.298 to 41.022)

Line C: $LC_{50} = 78.498$ ppm (range from 53.644 to 114.866)

- 30 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Novartis AG
- (B) STREET: Schwarzwaldallee 215
- (C) CITY: Basel
- (E) COUNTRY: Switzerland
- (F) POSTAL CODE (ZIP): 4002
- (G) TELEPHONE: +41 61 69 11 11
- (H) TELEFAX: + 41 61 696 79 76
- (I) TELEX: 962 991

(ii) TITLE OF INVENTION: Method of Controlling Insect Pests

(iii) NUMBER OF SEQUENCES: 55

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30B

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Bacillus cereus
- (B) STRAIN: AB78
- (C) INDIVIDUAL ISOLATE: NRRL B-21058

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1082..2467
- (D) OTHER INFORMATION: /product= "VIP2A(a)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

- 31 -

(B) LOCATION: 2475..5126

(D) OTHER INFORMATION: /note= "Coding sequence for the 100 kd VIPLA(a) protein. This coding sequence is repeated in SEQ ID NO:4 and translated separately."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATCGATACAA TGTGTGTTTA CTTAGACCGG TAGTCTCTGT AATTGTGTTA ATGCTATATT	60
CTTTACTTTG ATACATTTTA ATAGCCATTT CAACCTTATC AGTATGTTTT TGTGGTCTTC	120
CTCCTTTTTT TCCACGAGCT CTAGCTGCGT TTAATCCTGT TTTGGTACGT TCGCTAATAA	180
TATCTCTTTC TAATTCTGCA ATACTTGCCA TCATTGAAA GAAGAATTC OCCATAGCAT	240
TAGAGGTATC AATGTGTGCA TGAATAGAAA TAAATCTAC ACCTAGCTCT TTGAATTTTT	300
CACTTAATC AATTAGGTGT TTTGTAGAGC GAGAAATTCG ATCAAGTTTG TAAACAACCTA	360
TCTTATCGCC TTTACGTAAT ACTTTTAGCA ACTCTTCGAG TTGAGGGCGC TCTTTTTTTA	420
TTCTGTAT TTTCTCTGA TATAGCCTTT CTACACCATA TTGTGCAAA GCATCTATTT	480
GCATATCGAG ATTTTGTICT TCTGTGCTGA CACGAGCATA ACCAAAAATC AAATGGTTT	540
CACTTCCTAT CTAAATATAT CTATTAAAT AGCACCAAAA ACCTTATTAA ATTAAATAA	600
GGAACCTTGT TTTTGGATAT GGATTTTGGT ACTCAATATG GATGAGTTTT TAACGCTTTT	660
GTTAAAAAAC AAACAAGTGC CATAAACGGT CGTTTTTGGG ATGACATAAT AAATAATCTG	720
TTTGATTAAC CTAACCTTGT ATCCTTACAG CCCAGTTTTA TTGTACTTC AACTGACTGA	780
ATATGAAAAC AACATGAAGG TTTTATAAAA TTTATATATT TTCCATAACG GATGCTCTAT	840
CTTTAGGTTA TAGTTAAATT ATAAGAAAA AACAAACGGA GGGAGTGAAA AAAAGCATCT	900
TCTCTATAAT TTTACAGGCT CTTTAATAAG AAGGGGGGAG ATTAGATAAT AAATATGAAT	960
ATCTATCTAT AATTGTTTGC TTCTACAATA ACTTATCTAA CTTTCATATA CAACAACAAA	1020
ACAGACTAAA TCCAGATTGT ATATTCAATT TCAGTTGTTT CTTTATAAAA TAATTCATA	1080
A ATG AAA AGA ATG GAG GGA AAG TTG TTT ATG GTG TCA AAA AAA TTA	1126
Met Lys Arg Met Glu Gly Lys Leu Phe Met Val Ser Lys Lys Leu	
1 5 10 15	
CAA GTA GTT ACT AAA ACT GTA TTG CTT AGT ACA GTT TTC TCT ATA TCT	1174
Gln Val Val Thr Lys Thr Val Leu Leu Ser Thr Val Phe Ser Ile Ser	
20 25 30	
TTA TTA AAT AAT GAA GTG ATA AAA GCT GAA CAA TTA AAT ATA AAT TCT	1222
Leu Leu Asn Asn Glu Val Ile Lys Ala Glu Gln Leu Asn Ile Asn Ser	
35 40 45	
CAA AGT AAA TAT ACT AAC TTG CAA AAT CTA AAA ATC ACT GAC AAG GTA	1270

- 32 -

Gln	Ser	Lys	Tyr	Thr	Asn	Leu	Gln	Asn	Leu	Lys	Ile	Thr	Asp	Lys	Val	
		50					55					60				
GAG	GAT	TTT	AAA	GAA	GAT	AAG	GAA	AAA	GCG	AAA	GAA	TGG	GGG	AAA	GAA	1318
Glu	Asp	Phe	Lys	Glu	Asp	Lys	Glu	Lys	Ala	Lys	Glu	Trp	Gly	Lys	Glu	
		65				70					75					
AAA	GAA	AAA	GAG	TGG	AAA	CTA	ACT	GCT	ACT	GAA	AAA	GGA	AAA	ATG	AAT	1366
Lys	Glu	Lys	Glu	Trp	Lys	Leu	Thr	Ala	Thr	Glu	Lys	Gly	Lys	Met	Asn	
		80			85					90					95	
AAT	TTT	TTA	GAT	AAT	AAA	AAT	GAT	ATA	AAG	ACA	AAT	TAT	AAA	GAA	ATT	1414
Asn	Phe	Leu	Asp	Asn	Lys	Asn	Asp	Ile	Lys	Thr	Asn	Tyr	Lys	Glu	Ile	
				100				105						110		
ACT	TTT	TCT	ATG	GCA	GGC	TCA	TTT	GAA	GAT	GAA	ATA	AAA	GAT	TTA	AAA	1462
Thr	Phe	Ser	Met	Ala	Gly	Ser	Phe	Glu	Asp	Glu	Ile	Lys	Asp	Leu	Lys	
			115					120					125			
GAA	ATT	GAT	AAG	ATG	TTT	GAT	AAA	ACC	AAT	CTA	TCA	AAT	TCT	ATT	ATC	1510
Glu	Ile	Asp	Lys	Met	Phe	Asp	Lys	Thr	Asn	Leu	Ser	Asn	Ser	Ile	Ile	
		130					135				140					
ACC	TAT	AAA	AAT	GTG	GAA	CCG	ACA	ACA	ATT	GGA	TTT	AAT	AAA	TCT	TTA	1558
Thr	Tyr	Lys	Asn	Val	Glu	Pro	Thr	Thr	Ile	Gly	Phe	Asn	Lys	Ser	Leu	
		145				150					155					
ACA	GAA	GGT	AAT	ACG	ATT	AAT	TCT	GAT	GCA	ATG	GCA	CAG	TTT	AAA	GAA	1606
Thr	Glu	Gly	Asn	Thr	Ile	Asn	Ser	Asp	Ala	Met	Ala	Gln	Phe	Lys	Glu	
	160				165				170						175	
CAA	TTT	TTA	GAT	AGG	GAT	ATT	AAG	TTT	GAT	AGT	TAT	CTA	GAT	ACG	CAT	1654
Gln	Phe	Leu	Asp	Arg	Asp	Ile	Lys	Phe	Asp	Ser	Tyr	Leu	Asp	Thr	His	
				180					185					190		
TTA	ACT	GCT	CAA	CAA	GTT	TCC	AGT	AAA	GAA	AGA	GTT	ATT	TTG	AAG	GTT	1702
Leu	Thr	Ala	Gln	Gln	Val	Ser	Ser	Lys	Glu	Arg	Val	Ile	Leu	Lys	Val	
			195					200					205			
ACG	GTT	CCG	AGT	GGG	AAA	GGT	TCT	ACT	ACT	CCA	ACA	AAA	GCA	GGT	GTC	1750
Thr	Val	Pro	Ser	Gly	Lys	Gly	Ser	Thr	Thr	Pro	Thr	Lys	Ala	Gly	Val	
		210					215					220				
ATT	TTA	AAT	AAT	AGT	GAA	TAC	AAA	ATG	CTC	ATT	GAT	AAT	GGG	TAT	ATG	1798
Ile	Leu	Asn	Asn	Ser	Glu	Tyr	Lys	Met	Leu	Ile	Asp	Asn	Gly	Tyr	Met	
		225				230					235					
GTC	CAT	GTA	GAT	AAG	GTA	TCA	AAA	GTG	GTG	AAA	AAA	GGG	GTG	GAG	TGC	1846
Val	His	Val	Asp	Lys	Val	Ser	Lys	Val	Val	Lys	Lys	Gly	Val	Glu	Cys	
		240			245					250					255	
TTA	CAA	ATT	GAA	GGG	ACT	TTA	AAA	AAG	AGT	CTT	GAC	TTT	AAA	AAT	GAT	1894
Leu	Gln	Ile	Glu	Gly	Thr	Leu	Lys	Lys	Ser	Leu	Asp	Phe	Lys	Asn	Asp	
				260					265						270	

- 33 -

ATA AAT GCT GAA GCG CAT AGC TGG GGT ATG AAG AAT TAT GAA GAG TGG Ile Asn Ala Glu Ala His Ser Trp Gly Met Lys Asn Tyr Glu Glu Trp 275 280 285	1942
GCT AAA GAT TTA ACC GAT TCG CAA AGG GAA GCT TTA GAT GGG TAT GCT Ala Lys Asp Leu Thr Asp Ser Gln Arg Glu Ala Leu Asp Gly Tyr Ala 290 295 300	1990
AGG CAA GAT TAT AAA GAA ATC AAT AAT TAT TTA AGA AAT CAA GGC GGA Arg Gln Asp Tyr Lys Glu Ile Asn Asn Tyr Leu Arg Asn Gln Gly Gly 305 310 315	2038
AGT GGA AAT GAA AAA CTA GAT GCT CAA ATA AAA AAT ATT TCT GAT GCT Ser Gly Asn Glu Lys Leu Asp Ala Gln Ile Lys Asn Ile Ser Asp Ala 320 325 330 335	2086
TTA GGG AAG AAA CCA ATA CCG GAA AAT ATT ACT GTG TAT AGA TGG TGT Leu Gly Lys Lys Pro Ile Pro Glu Asn Ile Thr Val Tyr Arg Trp Cys 340 345 350	2134
GGC ATG CCG GAA TTT GGT TAT CAA ATT AGT GAT CCG TTA CCT TCT TTA Gly Met Pro Glu Phe Gly Tyr Gln Ile Ser Asp Pro Leu Pro Ser Leu 355 360 365	2182
AAA GAT TTT GAA GAA CAA TTT TTA AAT ACA ATC AAA GAA GAC AAA GGA Lys Asp Phe Glu Glu Gln Phe Leu Asn Thr Ile Lys Glu Asp Lys Gly 370 375 380	2230
TAT ATG AGT ACA AGC TTA TCG AGT GAA CGT CTT GCA GCT TTT GGA TCT Tyr Met Ser Thr Ser Leu Ser Ser Glu Arg Leu Ala Ala Phe Gly Ser 385 390 395	2278
AGA AAA ATT ATA TTA CGA TTA CAA GTT CCG AAA GGA AGT ACG GGT GCG Arg Lys Ile Ile Leu Arg Leu Gln Val Pro Lys Gly Ser Thr Gly Ala 400 405 410 415	2326
TAT TTA AGT GCC ATT GGT GGA TTT GCA AGT GAA AAA GAG ATC CTA CTT Tyr Leu Ser Ala Ile Gly Gly Phe Ala Ser Glu Lys Glu Ile Leu Leu 420 425 430	2374
GAT AAA GAT AGT AAA TAT CAT ATT GAT AAA GTA ACA GAG GTA ATT ATT Asp Lys Asp Ser Lys Tyr His Ile Asp Lys Val Thr Glu Val Ile Ile 435 440 445	2422
AAA GGT GTT AAG CGA TAT GTA GTG GAT GCA ACA TTA TTA ACA AAT Lys Gly Val Lys Arg Tyr Val Val Asp Ala Thr Leu Leu Thr Asn 450 455 460	2467
TAAGGAGATG AAAAAATATGA AGAAAAAGTT AGCAAGTGTT GTAACGTGTA CGTTATTAGC	2527
TCCTATGTTT TTGAATGGAA ATGTGAATGC TGTTTACGCA GACAGCAAAA CAAATCAAAT	2587
TTCTACAACA CAGAAAAATC AACAGAAAGA GATGGACCGA AAAGGATTAC TTGGGTATTA	2647
TTTCAAAGGA AAAGATTTTA GTAATCTTAC TATGTTTGCA CCGACACGTG ATAGTACTCT	2707

TATTTATGAT CAACAAACAG CAAATAAACT ATTAGATAAA AAACAACAAG AATATCAGTC	2767
TATTCGTTGG ATTGGTTTGA TTCAGAGTAA AGAAACGGGA GATTTACAT TTAACCTATC	2827
TGAGGATGAA CAGGCAATTA TAGAAATCAA TGGGAAAATT ATTTCTAATA AAGGGAAAGA	2887
AAAGCAAGTT GTCCATTTAG AAAAAGGAAA ATTAGTTCCA ATCAAAATAG AGTATCAATC	2947
AGATACAAA TTTAATATTG ACAGTAAAC ATTTAAAGAA CTTAAATTAT TTAAATAGA	3007
TAGTCAAAAC CAACCCAGC AAGTCCAGCA AGATGAACTG AGAAATCCTG AATTTAACAA	3067
GAAAGAATCA CAGGAATTCT TAGCGAAACC ATCGAAAATA AATCTTTTCA CTCAAAAAAT	3127
GAAAAGGGAA ATTGATGAAG ACACGGATAC GGATGGGGAC TCTATTCTG ACCTTTGGGA	3187
AGAAAATGGG TATACGATTC ACAATAGAAT CGCTGTAAAG TGGGACGATT CTCTAGCAAG	3247
TAAAGGGTAT ACGAAATTG TTTCAAATCC ACTAGAAAGT CACACAGTTG GTGATCCTTA	3307
TACAGATTAT GAAAAGGCAG CAAGAGATCT AGATTTGTCA AATGCAAAGG AAACGTTTAA	3367
CCCATGGTA GCTGCTTTTC CAAGTGTGAA TGTTAGTATG GAAAAGGTGA TATTATCACC	3427
AAATGAAAAT TTATCCAATA GTGTAGAGTC TCATTATCC ACGAATTGGT CTTATACAAA	3487
TACAGAAGGT GCTTCTGTG AAGCGGGAT TGGACCAAAA GGTATTTCTG TCGGAGTTAG	3547
CGTAACTAT CAACACTCTG AAACAGTTGC ACAAGAATGG GGAACATCTA CAGGAAATAC	3607
TTGCAATTC AATACGGCTT CAGCGGGATA TTTAAATGCA AATGTTGAT ATAACAATGT	3667
AGGAACTGGT GCCATCTACG ATGTAAAACC TACAACAAGT TTTGTATTAA ATAACGATAC	3727
TATCGCAACT ATTACGGCGA AATCTAATTC TACAGCCTTA AATATATCTC CTGGAGAAAG	3787
TTACCCGAAA AAAGGACAAA ATGGAATCGC AATAACATCA ATGGATGATT TTAATTCCCA	3847
TCCGATTACA TTAAATAAAA AACAAAGTAG TAATCTGCTA AATAATAAAC CTATGATGTT	3907
GGAAACAAAC CAAACAGATG GTGTTTATAA GATAAAAGAT ACACATGGAA ATATAGTAAC	3967
TGGCGGAGAA TGGAAATGGT TCATACAACA AATCAAGGCT AAAACAGCGT CTATTATTGT	4027
GGATGATGGG GAACGTGTAG CAGAAAAACG TGTAGCGCA AAAGATTATG AAAATCCAGA	4087
AGATAAAACA CCGTCTTTAA CTTTAAAAGA TGCCCTGAAG CTTTCATATC CAGATGAAAT	4147
AAAAGAAATA GAGGGATTAT TATATTATAA AAACAAACCG ATATACGAAT CGAGCGTTAT	4207
GACTTACTTA GATGAAAATA CAGCAAAAGA AGTGACCAAA CAATTAAATG ATACCACTGG	4267
GAAATTTAAA GATGTAAGTC ATTTATATGA TGTAAAACTG ACTCCAAAAA TGAATGTTAC	4327

AATCAAATIG TCTATACTTT ATGATAATGC TGAGTCTAAT GATAACTCAA TTGGTAAATG	4387
GACAAACACA AATATTGTTT CAGGTGGAAA TAACGGAAAA AAACAATATT CTTCTAATAA	4447
TCCGGATGCT AATTTGACAT TAAATACAGA TGCTCAAGAA AAATTAAATA AAAATCGTGA	4507
CTATTATATA AGTTTATATA TGAAGTCAGA AAAAAACACA CAATGTGAGA TTTACTATAGA	4567
TGGGGAGATT TATCCGATCA CTACAAAAAC AGTGAATGTG AATAAAGACA ATTACAAAAG	4627
ATTAGATATT ATAGCTCATA ATATAAAAAG TAATCCAATT TCTTCACTTC ATATTAAAAC	4687
GAATGATGAA ATAACTTTAT TTTGGGATGA TATTTCTATA ACAGATGTAG CATCAATAAA	4747
ACCGGAAAAT TTAACAGATT CAGAAATTAA ACAGATTTAT AGTAGGTATG GTATTAAAGT	4807
AGAAGATGGA ATCCTTATTG ATAAAAAAGG TGGGATTCAT TATGGTGAAT TTATTAATGA	4867
AGCTAGTTTT AATATTGAAC CATTGCAAAA TTATGTGACC AAATATGAAG TTACTTATAG	4927
TAGTGAGTTA GGACCAAACG TGAGTGACAC ACTTGAAAGT GATAAAATTT ACAAGGATGG	4987
GACAATTAAA TTTGATTTTA CCAAATATAG TAAAAATGAA CAAGGATTAT TTTATGACAG	5047
TGGATTAAAT TGGGACTTTA AAATTAATGC TATTACTTAT GATGGTAAAG AGATGAATGT	5107
TTTTCATAGA TATAATAAAT AGTTATTATA TCTATGAAGC TGGTGCTAAA GATAGTGTA	5167
AAGTTAATAT ACTGTAGGAT TGTAATAAAA GTAATGGAAT TGATATCGTA CTTTGGAGTG	5227
GGGGATACTT TGTAATAGT TCTATCAGAA ACATTAGACT AAGAAAAGTT ACTACCCCCA	5287
CTTGAAAATG AAGATTCAAC TGATTACAAA CAACCTGTTA AATATTATAA GGTTTTAACA	5347
AAATATTAAA CTCTTTATGT TAATACTGTA ATATAAAGAG TTTAATTGTA TTCAAATGAA	5407
GCTTTCCAC AAAATTAGAC TGATTATCTA ATGAAATAAT CAGTCTAATT TTGTAGAACA	5467
GGTCTGGTAT TATTGTACGT GGTCACTAAA AGATATCTAA TATTATTGGG CAAGGCGTTC	5527
CATGATTGAA TCCTCGAATG TCTTGCCCTT TTCATTTATT TAAGAAGGAT TGTGGAGAAA	5587
TTATGGTTTA GATAATGAAG AAAGACTTCA CTTCTAATTT TTGATGTTAA ATAAATCAAA	5647
ATTTGGCGAT TCACATTGTT TAATCCACTG ATAAAACATA CTGGAGIGTT CTTAAAAAAT	5707
CAGCTTTTTT CTTTATAAAA TTTTGCTTAG CGTACGAAAT TCGTGTMTTG TTGGTGGGAC	5767
CCCATGCCCA TCAACTTAAG AGTAAATTAG TAATGAACIT TCGTTCATCT GGATTAAAAT	5827
AACCTCAAAT TAGGACATGT TTTTAAAAAT AAGCAGACCA AATAAGCCTA GAATAGGTAT	5887
CATTTTTTAAA AATTATGCTG CTTTCTTTTG TTTTCCAAAT CCATTATACT CATAAGCAAC	5947
ACCCATAATG TCAAAGACTG TTTTGTCTC ATATCGATAA GCTTGATATC GAATTCCTGC	6007

AGCCCCGGGG ATCCACTAGT TCTAGAGCGG CGCCACCGC GG

6049

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Met Lys Arg Met Glu Gly Lys Leu Phe Met Val Ser Lys Lys Leu Gln
 1             5             10             15
Val Val Thr Lys Thr Val Leu Leu Ser Thr Val Phe Ser Ile Ser Leu
          20             25             30
Leu Asn Asn Glu Val Ile Lys Ala Glu Gln Leu Asn Ile Asn Ser Gln
          35             40             45
Ser Lys Tyr Thr Asn Leu Gln Asn Leu Lys Ile Thr Asp Lys Val Glu
          50             55             60
Asp Phe Lys Glu Asp Lys Glu Lys Ala Lys Glu Trp Gly Lys Glu Lys
          65             70             75             80
Glu Lys Glu Trp Lys Leu Thr Ala Thr Glu Lys Gly Lys Met Asn Asn
          85             90             95
Phe Leu Asp Asn Lys Asn Asp Ile Lys Thr Asn Tyr Lys Glu Ile Thr
          100            105            110
Phe Ser Met Ala Gly Ser Phe Glu Asp Glu Ile Lys Asp Leu Lys Glu
          115            120            125
Ile Asp Lys Met Phe Asp Lys Thr Asn Leu Ser Asn Ser Ile Ile Thr
          130            135            140
Tyr Lys Asn Val Glu Pro Thr Thr Ile Gly Phe Asn Lys Ser Leu Thr
          145            150            155            160
Glu Gly Asn Thr Ile Asn Ser Asp Ala Met Ala Gln Phe Lys Glu Gln
          165            170            175
Phe Leu Asp Arg Asp Ile Lys Phe Asp Ser Tyr Leu Asp Thr His Leu
          180            185            190
Thr Ala Gln Gln Val Ser Ser Lys Glu Arg Val Ile Leu Lys Val Thr
          195            200            205
Val Pro Ser Gly Lys Gly Ser Thr Thr Pro Thr Lys Ala Gly Val Ile

```

- 37 -

210	215	220
Leu Asn Asn Ser Glu Tyr Lys Met Leu Ile Asp Asn Gly Tyr Met Val		
225	230	235 240
His Val Asp Lys Val Ser Lys Val Val Lys Lys Gly Val Glu Cys Leu		
	245	250 255
Gln Ile Glu Gly Thr Leu Lys Lys Ser Leu Asp Phe Lys Asn Asp Ile		
	260	265 270
Asn Ala Glu Ala His Ser Trp Gly Met Lys Asn Tyr Glu Glu Trp Ala		
	275	280 285
Lys Asp Leu Thr Asp Ser Gln Arg Glu Ala Leu Asp Gly Tyr Ala Arg		
	290	295 300
Gln Asp Tyr Lys Glu Ile Asn Asn Tyr Leu Arg Asn Gln Gly Gly Ser		
305	310	315 320
Gly Asn Glu Lys Leu Asp Ala Gln Ile Lys Asn Ile Ser Asp Ala Leu		
	325	330 335
Gly Lys Lys Pro Ile Pro Glu Asn Ile Thr Val Tyr Arg Trp Cys Gly		
	340	345 350
Met Pro Glu Phe Gly Tyr Gln Ile Ser Asp Pro Leu Pro Ser Leu Lys		
	355	360 365
Asp Phe Glu Glu Gln Phe Leu Asn Thr Ile Lys Glu Asp Lys Gly Tyr		
	370	375 380
Met Ser Thr Ser Leu Ser Ser Glu Arg Leu Ala Ala Phe Gly Ser Arg		
385	390	395 400
Lys Ile Ile Leu Arg Leu Gln Val Pro Lys Gly Ser Thr Gly Ala Tyr		
	405	410 415
Leu Ser Ala Ile Gly Gly Phe Ala Ser Glu Lys Glu Ile Leu Leu Asp		
	420	425 430
Lys Asp Ser Lys Tyr His Ile Asp Lys Val Thr Glu Val Ile Ile Lys		
	435	440 445
Gly Val Lys Arg Tyr Val Val Asp Ala Thr Leu Leu Thr Asn		
	450	455 460

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- 38 -

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Signal peptide for vacuolar targetting"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

Ser Ser Ser Ser Phe Ala Asp Ser Asn Pro Ile Arg Val Thr Asp Arg
1           5           10           15
Ala Ala Ser Thr
                20

```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Bacillus cereus
- (B) STRAIN: AB78
- (C) INDIVIDUAL ISOLATE: NRRL B-21058

(ix) FEATURE:

- (A) NAME/KEY: CDS
 - (B) LOCATION: 1..2652
 - (D) OTHER INFORMATION: /product= "100 kDa protein VIP1A(a)"
- /note= "This sequence is identical to the portion of SEQ ID NO:1 between and including nucleotide 2475 to 5126."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

ATG AAA AAT ATG AAG AAA AAG TTA GCA AGT GTT GTA ACG TGT ACG TTA      48
Met Lys Asn Met Lys Lys Lys Leu Ala Ser Val Val Thr Cys Thr Leu
    465                470                475

TTA GCT CCT ATG TTT TTG AAT GGA AAT GTG AAT GCT GTT TAC GCA GAC      96
Leu Ala Pro Met Phe Leu Asn Gly Asn Val Asn Ala Val Tyr Ala Asp
    480                485                490

```

- 39 -

AGC AAA ACA AAT CAA ATT TCT ACA ACA CAG AAA AAT CAA CAG AAA GAG Ser Lys Thr Asn Gln Ile Ser Thr Thr Gln Lys Asn Gln Gln Lys Glu 495 500 505 510	144
ATG GAC CGA AAA GGA TTA CTT GGG TAT TAT TTC AAA GGA AAA GAT TTT Met Asp Arg Lys Gly Leu Leu Gly Tyr Tyr Phe Lys Gly Lys Asp Phe 515 520 525	192
AGT AAT CTT ACT ATG TTT GCA CCG ACA CGT GAT AGT ACT CTT ATT TAT Ser Asn Leu Thr Met Phe Ala Pro Thr Arg Asp Ser Thr Leu Ile Tyr 530 535 540	240
GAT CAA CAA ACA GCA AAT AAA CTA TTA GAT AAA AAA CAA CAA GAA TAT Asp Gln Gln Thr Ala Asn Lys Leu Leu Asp Lys Lys Gln Gln Glu Tyr 545 550 555	288
CAG TCT ATT CGT TGG ATT GGT TTG ATT CAG AGT AAA GAA ACG GGA GAT Gln Ser Ile Arg Trp Ile Gly Leu Ile Gln Ser Lys Glu Thr Gly Asp 560 565 570	336
TTC ACA TTT AAC TTA TCT GAG GAT GAA CAG GCA ATT ATA GAA ATC AAT Phe Thr Phe Asn Leu Ser Glu Asp Glu Gln Ala Ile Ile Glu Ile Asn 575 580 585 590	384
GGG AAA ATT ATT TCT AAT AAA GGG AAA GAA AAG CAA GTT GTC CAT TTA Gly Lys Ile Ile Ser Asn Lys Gly Lys Glu Lys Gln Val Val His Leu 595 600 605	432
GAA AAA GGA AAA TTA GTT CCA ATC AAA ATA GAG TAT CAA TCA GAT ACA Glu Lys Gly Lys Leu Val Pro Ile Lys Ile Glu Tyr Gln Ser Asp Thr 610 615 620	480
AAA TTT AAT ATT GAC AGT AAA ACA TTT AAA GAA CTT AAA TTA TTT AAA Lys Phe Asn Ile Asp Ser Lys Thr Phe Lys Glu Leu Lys Leu Phe Lys 625 630 635	528
ATA GAT AGT CAA AAC CAA CCC CAG CAA GTC CAG CAA GAT GAA CTG AGA Ile Asp Ser Gln Asn Gln Pro Gln Gln Val Gln Gln Asp Glu Leu Arg 640 645 650	576
AAT CCT GAA TTT AAC AAG AAA GAA TCA CAG GAA TTC TTA GCG AAA CCA Asn Pro Glu Phe Asn Lys Lys Glu Ser Gln Glu Phe Leu Ala Lys Pro 655 660 665 670	624
TCG AAA ATA AAT CTT TTC ACT CAA AAA ATG AAA AGG GAA ATT GAT GAA Ser Lys Ile Asn Leu Phe Thr Gln Lys Met Lys Arg Glu Ile Asp Glu 675 680 685	672
GAC ACG GAT ACG GAT GGG GAC TCT ATT CCT GAC CTT TGG GAA GAA AAT Asp Thr Asp Thr Asp Gly Asp Ser Ile Pro Asp Leu Trp Glu Glu Asn 690 695 700	720
GGG TAT ACG ATT CAA AAT AGA ATC GCT GTA AAG TGG GAC GAT TCT CTA Gly Tyr Thr Ile Gln Asn Arg Ile Ala Val Lys Trp Asp Asp Ser Leu 705 710 715	768

- 40 -

GCA AGT AAA GGG TAT ACG AAA TTT GTT TCA AAT CCA CTA GAA AGT CAC Ala Ser Lys Gly Tyr Thr Lys Phe Val Ser Asn Pro Leu Glu Ser His 720 725 730	816
ACA GTT GGT GAT CCT TAT ACA GAT TAT GAA AAG GCA GCA AGA GAT CTA Thr Val Gly Asp Pro Tyr Thr Asp Tyr Glu Lys Ala Ala Arg Asp Leu 735 740 745 750	864
GAT TTG TCA AAT GCA AAG GAA ACG TTT AAC CCA TTG GTA GCT GCT TTT Asp Leu Ser Asn Ala Lys Glu Thr Phe Asn Pro Leu Val Ala Ala Phe 755 760 765	912
CCA AGT GTG AAT GTT AGT ATG GAA AAG GTG ATA TTA TCA CCA AAT GAA Pro Ser Val Asn Val Ser Met Glu Lys Val Ile Leu Ser Pro Asn Glu 770 775 780	960
AAT TTA TCC AAT AGT GTA GAG TCT CAT TCA TCC ACG AAT TGG TCT TAT Asn Leu Ser Asn Ser Val Glu Ser His Ser Ser Thr Asn Trp Ser Tyr 785 790 795	1008
ACA AAT ACA GAA GGT GCT TCT GTT GAA GCG GGG ATT GGA CCA AAA GGT Thr Asn Thr Glu Gly Ala Ser Val Glu Ala Gly Ile Gly Pro Lys Gly 800 805 810	1056
ATT TCG TTC GGA GTT AGC GTA AAC TAT CAA CAC TCT GAA ACA GTT GCA Ile Ser Phe Gly Val Ser Val Asn Tyr Gln His Ser Glu Thr Val Ala 815 820 825 830	1104
CAA GAA TGG GGA ACA TCT ACA GGA AAT ACT TCG CAA TTC AAT ACG GCT Gln Glu Trp Gly Thr Ser Thr Gly Asn Thr Ser Gln Phe Asn Thr Ala 835 840 845	1152
TCA GCG GGA TAT TTA AAT GCA AAT GTT CGA TAT AAC AAT GTA GGA ACT Ser Ala Gly Tyr Leu Asn Ala Asn Val Arg Tyr Asn Asn Val Gly Thr 850 855 860	1200
GGT GCC ATC TAC GAT GTA AAA CCT ACA ACA AGT TTT GTA TTA AAT AAC Gly Ala Ile Tyr Asp Val Lys Pro Thr Thr Ser Phe Val Leu Asn Asn 865 870 875	1248
GAT ACT ATC GCA ACT ATT ACG GCG AAA TCT AAT TCT ACA GCC TTA AAT Asp Thr Ile Ala Thr Ile Thr Ala Lys Ser Asn Ser Thr Ala Leu Asn 880 885 890	1296
ATA TCT CCT GGA GAA AGT TAC CCG AAA AAA GGA CAA AAT GGA ATC GCA Ile Ser Pro Gly Glu Ser Tyr Pro Lys Lys Gly Gln Asn Gly Ile Ala 895 900 905 910	1344
ATA ACA TCA ATG GAT GAT TTT AAT TCC CAT CCG ATT ACA TTA AAT AAA Ile Thr Ser Met Asp Asp Phe Asn Ser His Pro Ile Thr Leu Asn Lys 915 920 925	1392
AAA CAA GTA GAT AAT CTG CTA AAT AAT AAA CCT ATG ATG TTG GAA ACA Lys Gln Val Asp Asn Leu Leu Asn Asn Lys Pro Met Met Leu Glu Thr 930 935 940 945 950	1440

- 41 -

930	935	940	
AAC CAA ACA GAT GGT GTT TAT AAG ATA AAA GAT ACA CAT GGA AAT ATA Asn Gln Thr Asp Gly Val Tyr Lys Ile Lys Asp Thr His Gly Asn Ile 945 950 955			1488
GTA ACT GGC GGA GAA TGG AAT GGT GTC ATA CAA CAA ATC AAG GCT AAA Val Thr Gly Gly Glu Trp Asn Gly Val Ile Gln Gln Ile Lys Ala Lys 960 965 970			1536
ACA GCG TCT ATT ATT GTG GAT GAT GGG GAA CGT GTA GCA GAA AAA CGT Thr Ala Ser Ile Ile Val Asp Asp Gly Glu Arg Val Ala Glu Lys Arg 975 980 985 990			1584
GTA GCG GCA AAA GAT TAT GAA AAT CCA GAA GAT AAA ACA CCG TCT TTA Val Ala Ala Lys Asp Tyr Glu Asn Pro Glu Asp Lys Thr Pro Ser Leu 995 1000 1005			1632
ACT TTA AAA GAT GCC CTG AAG CTT TCA TAT CCA GAT GAA ATA AAA GAA Thr Leu Lys Asp Ala Leu Lys Leu Ser Tyr Pro Asp Glu Ile Lys Glu 1010 1015 1020			1680
ATA GAG GGA TTA TTA TAT TAT AAA AAC AAA CCG ATA TAC GAA TCG AGC Ile Glu Gly Leu Leu Tyr Tyr Lys Asn Lys Pro Ile Tyr Glu Ser Ser 1025 1030 1035			1728
GTT ATG ACT TAC TTA GAT GAA AAT ACA GCA AAA GAA GTG ACC AAA CAA Val Met Thr Tyr Leu Asp Glu Asn Thr Ala Lys Glu Val Thr Lys Gln 1040 1045 1050			1776
TTA AAT GAT ACC ACT GGG AAA TTT AAA GAT GTA AGT CAT TTA TAT GAT Leu Asn Asp Thr Thr Gly Lys Phe Lys Asp Val Ser His Leu Tyr Asp 1055 1060 1065 1070			1824
GTA AAA CTG ACT CCA AAA ATG AAT GTT ACA ATC AAA TTG TCT ATA CTT Val Lys Leu Thr Pro Lys Met Asn Val Thr Ile Lys Leu Ser Ile Leu 1075 1080 1085			1872
TAT GAT AAT GCT GAG TCT AAT GAT AAC TCA ATT GGT AAA TGG ACA AAC Tyr Asp Asn Ala Glu Ser Asn Asp Asn Ser Ile Gly Lys Trp Thr Asn 1090 1095 1100			1920
ACA AAT ATT GTT TCA GGT GGA AAT AAC GGA AAA AAA CAA TAT TCT TCT Thr Asn Ile Val Ser Gly Gly Asn Asn Gly Lys Lys Gln Tyr Ser Ser 1105 1110 1115			1968
AAT AAT CCG GAT GCT AAT TTG ACA TTA AAT ACA GAT GCT CAA GAA AAA Asn Asn Pro Asp Ala Asn Leu Thr Leu Asn Thr Asp Ala Gln Glu Lys 1120 1125 1130			2016
TTA AAT AAA AAT CGT GAC TAT TAT ATA AGT TTA TAT ATG AAG TCA GAA Leu Asn Lys Asn Arg Asp Tyr Tyr Ile Ser Leu Tyr Met Lys Ser Glu 1135 1140 1145 1150			2064
AAA AAC ACA CAA TGT GAG ATT ACT ATA GAT GGG GAG ATT TAT CCG ATC			2112

- 42 -

Lys Asn Thr Gln Cys Glu Ile Thr Ile Asp Gly Glu Ile Tyr Pro Ile	
1155 1160 1165	
ACT ACA AAA ACA GTG AAT GTG AAT AAA GAC AAT TAC AAA AGA TTA GAT	2160
Thr Thr Lys Thr Val Asn Val Asn Lys Asp Asn Tyr Lys Arg Leu Asp	
1170 1175 1180	
ATT ATA GCT CAT AAT ATA AAA AGT AAT CCA ATT TCT TCA CTT CAT ATT	2208
Ile Ile Ala His Asn Ile Lys Ser Asn Pro Ile Ser Ser Leu His Ile	
1185 1190 1195	
AAA ACG AAT GAT GAA ATA ACT TTA TTT TGG GAT GAT ATT TCT ATA ACA	2256
Lys Thr Asn Asp Glu Ile Thr Leu Phe Trp Asp Ile Ser Ile Thr	
1200 1205 1210	
GAT GTA GCA TCA ATA AAA CCG GAA AAT TTA ACA GAT TCA GAA ATT AAA	2304
Asp Val Ala Ser Ile Lys Pro Glu Asn Leu Thr Asp Ser Glu Ile Lys	
1215 1220 1225 1230	
CAG ATT TAT AGT AGG TAT GGT ATT AAG TTA GAA GAT GGA ATC CTT ATT	2352
Gln Ile Tyr Ser Arg Tyr Gly Ile Lys Leu Glu Asp Gly Ile Leu Ile	
1235 1240 1245	
GAT AAA AAA GGT GGG ATT CAT TAT GGT GAA TTT ATT AAT GAA GCT AGT	2400
Asp Lys Lys Gly Gly Ile His Tyr Gly Glu Phe Ile Asn Glu Ala Ser	
1250 1255 1260	
TTT AAT ATT GAA CCA TTG CAA AAT TAT GTG ACC AAA TAT GAA GTT ACT	2448
Phe Asn Ile Glu Pro Leu Gln Asn Tyr Val Thr Lys Tyr Glu Val Thr	
1265 1270 1275	
TAT AGT AGT GAG TTA GGA CCA AAC GTG AGT GAC ACA CTT GAA AGT GAT	2496
Tyr Ser Ser Glu Leu Gly Pro Asn Val Ser Asp Thr Leu Glu Ser Asp	
1280 1285 1290	
AAA ATT TAC AAG GAT GGG ACA ATT AAA TTT GAT TTT ACC AAA TAT AGT	2544
Lys Ile Tyr Lys Asp Gly Thr Ile Lys Phe Asp Phe Thr Lys Tyr Ser	
1295 1300 1305 1310	
AAA AAT GAA CAA GGA TTA TTT TAT GAC AGT GGA TTA AAT TGG GAC TTT	2592
Lys Asn Glu-Gln Gly Leu Phe Tyr Asp Ser Gly Leu Asn Trp Asp Phe	
1315 1320 1325	
AAA ATT AAT GCT ATT ACT TAT GAT GGT AAA GAG ATG AAT GTT TTT CAT	2640
Lys Ile Asn Ala Ile Thr Tyr Asp Gly Lys Glu Met Asn Val Phe His	
1330 1335 1340	
AGA TAT AAT AAA TAG	2655
Arg Tyr Asn Lys	
1345	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- 43 -

(A) LENGTH: 884 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

Met Lys Asn Met Lys Lys Lys Leu Ala Ser Val Val Thr Cys Thr Leu
 1             5             10             15
— Leu Ala Pro Met Phe Leu Asn Gly Asn Val Asn Ala Val Tyr Ala Asp
      20             25             30
Ser Lys Thr Asn Gln Ile Ser Thr Thr Gln Lys Asn Gln Gln Lys Glu
 35             40             45
Met Asp Arg Lys Gly Leu Leu Gly Tyr Tyr Phe Lys Gly Lys Asp Phe
 50             55             60
Ser Asn Leu Thr Met Phe Ala Pro Thr Arg Asp Ser Thr Leu Ile Tyr
 65             70             75             80
Asp Gln Gln Thr Ala Asn Lys Leu Leu Asp Lys Lys Gln Gln Glu Tyr
      85             90             95
Gln Ser Ile Arg Trp Ile Gly Leu Ile Gln Ser Lys Glu Thr Gly Asp
      100             105             110
Phe Thr Phe Asn Leu Ser Glu Asp Glu Gln Ala Ile Ile Glu Ile Asn
      115             120             125
Gly Lys Ile Ile Ser Asn Lys Gly Lys Glu Lys Gln Val Val His Leu
      130             135             140
Glu Lys Gly Lys Leu Val Pro Ile Lys Ile Glu Tyr Gln Ser Asp Thr
      145             150             155             160
Lys Phe Asn Ile Asp Ser Lys Thr Phe Lys Glu Leu Lys Leu Phe Lys
      165             170             175
Ile Asp Ser Gln Asn Gln Pro Gln Gln Val Gln Gln Asp Glu Leu Arg
      180             185             190
Asn Pro Glu Phe Asn Lys Lys Glu Ser Gln Glu Phe Leu Ala Lys Pro
      195             200             205
Ser Lys Ile Asn Leu Phe Thr Gln Lys Met Lys Arg Glu Ile Asp Glu
      210             215             220
Asp Thr Asp Thr Asp Gly Asp Ser Ile Pro Asp Leu Trp Glu Glu Asn
      225             230             235             240
Gly Tyr Thr Ile Gln Asn Arg Ile Ala Val Lys Trp Asp Asp Ser Leu
      245             250             255

```

- 44 -

Ala Ser Lys Gly Tyr Thr Lys Phe Val Ser Asn Pro Leu Glu Ser His
 260 265 270
 Thr Val Gly Asp Pro Tyr Thr Asp Tyr Glu Lys Ala Ala Arg Asp Leu
 275 280 285
 Asp Leu Ser Asn Ala Lys Glu Thr Phe Asn Pro Leu Val Ala Ala Phe
 290 295 300
 Pro Ser Val Asn Val Ser Met Glu Lys Val Ile Leu Ser Pro Asn Glu
 305 310 315 320
 Asn Leu Ser Asn Ser Val Glu Ser His Ser Ser Thr Asn Trp Ser Tyr
 325 330 335
 Thr Asn Thr Glu Gly Ala Ser Val Glu Ala Gly Ile Gly Pro Lys Gly
 340 345 350
 Ile Ser Phe Gly Val Ser Val Asn Tyr Gln His Ser Glu Thr Val Ala
 355 360 365
 Gln Glu Trp Gly Thr Ser Thr Gly Asn Thr Ser Gln Phe Asn Thr Ala
 370 375 380
 Ser Ala Gly Tyr Leu Asn Ala Asn Val Arg Tyr Asn Asn Val Gly Thr
 385 390 395 400
 Gly Ala Ile Tyr Asp Val Lys Pro Thr Thr Ser Phe Val Leu Asn Asn
 405 410 415
 Asp Thr Ile Ala Thr Ile Thr Ala Lys Ser Asn Ser Thr Ala Leu Asn
 420 425 430
 Ile Ser Pro Gly Glu Ser Tyr Pro Lys Lys Gly Gln Asn Gly Ile Ala
 435 440 445
 Ile Thr Ser Met Asp Asp Phe Asn Ser His Pro Ile Thr Leu Asn Lys
 450 455 460
 Lys Gln Val Asp Asn Leu Leu Asn Asn Lys Pro Met Met Leu Glu Thr
 465 470 475 480
 Asn Gln Thr Asp Gly Val Tyr Lys Ile Lys Asp Thr His Gly Asn Ile
 485 490 495
 Val Thr Gly Gly Glu Trp Asn Gly Val Ile Gln Gln Ile Lys Ala Lys
 500 505 510
 Thr Ala Ser Ile Ile Val Asp Asp Gly Glu Arg Val Ala Glu Lys Arg
 515 520 525
 Val Ala Ala Lys Asp Tyr Glu Asn Pro Glu Asp Lys Thr Pro Ser Leu
 530 535 540

- 45 -

Thr Leu Lys Asp Ala Leu Lys Leu Ser Tyr Pro Asp Glu Ile Lys Glu
 545 550 555 560
 Ile Glu Gly Leu Leu Tyr Tyr Lys Asn Lys Pro Ile Tyr Glu Ser Ser
 565 570 575
 Val Met Thr Tyr Leu Asp Glu Asn Thr Ala Lys Glu Val Thr Lys Gln
 580 585 590
 Leu Asn Asp Thr Thr Gly Lys Phe Lys Asp Val Ser His Leu Tyr Asp
 595 600 605
 Val Lys Leu Thr Pro Lys Met Asn Val Thr Ile Lys Leu Ser Ile Leu
 610 615 620
 Tyr Asp Asn Ala Glu Ser Asn Asp Asn Ser Ile Gly Lys Trp Thr Asn
 625 630 635 640
 Thr Asn Ile Val Ser Gly Gly Asn Asn Gly Lys Lys Gln Tyr Ser Ser
 645 650 655
 Asn Asn Pro Asp Ala Asn Leu Thr Leu Asn Thr Asp Ala Gln Glu Lys
 660 665 670
 Leu Asn Lys Asn Arg Asp Tyr Tyr Ile Ser Leu Tyr Met Lys Ser Glu
 675 680 685
 Lys Asn Thr Gln Cys Glu Ile Thr Ile Asp Gly Glu Ile Tyr Pro Ile
 690 695 700
 Thr Thr Lys Thr Val Asn Val Asn Lys Asp Asn Tyr Lys Arg Leu Asp
 705 710 715 720
 Ile Ile Ala His Asn Ile Lys Ser Asn Pro Ile Ser Ser Leu His Ile
 725 730 735
 Lys Thr Asn Asp Glu Ile Thr Leu Phe Trp Asp Asp Ile Ser Ile Thr
 740 745 750
 Asp Val Ala Ser Ile Lys Pro Glu Asn Leu Thr Asp Ser Glu Ile Lys
 755 760 765
 Gln Ile Tyr Ser Arg Tyr Gly Ile Lys Leu Glu Asp Gly Ile Leu Ile
 770 775 780
 Asp Lys Lys Gly Gly Ile His Tyr Gly Glu Phe Ile Asn Glu Ala Ser
 785 790 795 800
 Phe Asn Ile Glu Pro Leu Gln Asn Tyr Val Thr Lys Tyr Glu Val Thr
 805 810 815
 Tyr Ser Ser Glu Leu Gly Pro Asn Val Ser Asp Thr Leu Glu Ser Asp
 820 825 830
 Lys Ile Tyr Lys Asp Gly Thr Ile Lys Phe Asp Phe Thr Lys Tyr Ser

835					840					845					
Lys	Asn	Glu	Gln	Gly	Leu	Phe	Tyr	Asp	Ser	Gly	Leu	Asn	Trp	Asp	Phe
850					855					860					
Lys	Ile	Asn	Ala	Ile	Thr	Tyr	Asp	Gly	Lys	Glu	Met	Asn	Val	Phe	His
865					870					875					880
Arg Tyr Asn Lys															

(2) INFORMATION FOR SEQ ID NO:6:

- ```

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2004 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Bacillus cereus
 (B) STRAIN: AB78
 (C) INDIVIDUAL ISOLATE: NRRL B-21058

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..2001
 (D) OTHER INFORMATION: /product= "80 kDa protein VPI1A(a)"
/note= "This sequence is identical to that found in SEQ ID NO:1
between and including nucleotide positions 3126 and 5126"

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG AAA AGG GAA ATT GAT GAA GAC ACG GAT ACG GAT GGG GAC TCT ATT | 48  |
| Met Lys Arg Glu Ile Asp Glu Asp Thr Asp Thr Asp Gly Asp Ser Ile |     |
| 885 890 895 900                                                 |     |
| CCT GAC CTT TGG GAA GAA AAT GGG TAT ACG ATT CAA AAT AGA ATC GCT | 96  |
| Pro Asp Leu Trp Glu Glu Asn Gly Tyr Thr Ile Gln Asn Arg Ile Ala |     |
| 905 910 915                                                     |     |
| GTA AAG TGG GAC GAT TCT CTA GCA AGT AAA GGG TAT ACG AAA TTT GTT | 144 |
| Val Lys Trp Asp Asp Ser Leu Ala Ser Lys Gly Tyr Thr Lys Phe Val |     |
| 920 925 930                                                     |     |
| TCA AAT CCA CTA GAA AGT CAC ACA GTT GGT GAT CCT TAT ACA GAT TAT | 192 |
| Ser Asn Pro Leu Glu Ser His Thr Val Gly Asp Pro Tyr Thr Asp Tyr |     |
| 935 940 945                                                     |     |

|                                                                                                                                                           |     |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| GAA AAG GCA GCA AGA GAT CTA GAT TTG TCA AAT GCA AAG GAA ACG TTT<br>Glu Lys Ala Ala Arg Asp Leu Asp Leu Ser Asn Ala Lys Glu Thr Phe<br>950 955 960         | 240 |
| AAC CCA TTG GTA GCT GCT TTT CCA AGT GTG AAT GTT AGT ATG GAA AAG<br>Asn Pro Leu Val Ala Ala Phe Pro Ser Val Asn Val Ser Met Glu Lys<br>965 970 975 980     | 288 |
| GTG ATA TTA TCA CCA AAT GAA AAT TTA TCC AAT AGT GTA GAG TCT CAT<br>Val Ile Leu Ser Pro Asn Glu Asn Leu Ser Asn Ser Val Glu Ser His<br>985 990 995         | 336 |
| TCA TCC ACG AAT TGG TCT TAT ACA AAT ACA GAA GGT GCT TCT GTT GAA<br>Ser Ser Thr Asn Trp Ser Tyr Thr Asn Thr Glu Gly Ala Ser Val Glu<br>1000 1005 1010      | 384 |
| GCG GGG ATT GGA CCA AAA GGT ATT TCG TTC GGA GTT AGC GTA AAC TAT<br>Ala Gly Ile Gly Pro Lys Gly Ile Ser Phe Gly Val Ser Val Asn Tyr<br>1015 1020 1025      | 432 |
| CAA CAC TCT GAA ACA GTT GCA CAA GAA TGG GGA ACA TCT ACA GGA AAT<br>Gln His Ser Glu Thr Val Ala Gln Glu Trp Gly Thr Ser Thr Gly Asn<br>1030 1035 1040      | 480 |
| ACT TCG CAA TTC AAT ACG GCT TCA GCG GGA TAT TTA AAT GCA AAT GTT<br>Thr Ser Gln Phe Asn Thr Ala Ser Ala Gly Tyr Leu Asn Ala Asn Val<br>1045 1050 1055 1060 | 528 |
| CGA TAT AAC AAT GTA GGA ACT GGT GCC ATC TAC GAT GTA AAA CCT ACA<br>Arg Tyr Asn Asn Val Gly Thr Gly Ala Ile Tyr Asp Val Lys Pro Thr<br>1065 1070 1075      | 576 |
| ACA AGT TTT GTA TTA AAT AAC GAT ACT ATC GCA ACT ATT ACG GCG AAA<br>Thr Ser Phe Val Leu Asn Asn Asp Thr Ile Ala Thr Ile Thr Ala Lys<br>1080 1085 1090      | 624 |
| TCT AAT TCT ACA GCC TTA AAT ATA TCT CCT GGA GAA AGT TAC CCG AAA<br>Ser Asn Ser Thr Ala Leu Asn Ile Ser Pro Gly Glu Ser Tyr Pro Lys<br>1095 1100 1105      | 672 |
| AAA GGA CAA AAT GGA ATC GCA ATA ACA TCA ATG GAT GAT TTT AAT TCC<br>Lys Gly Gln Asn Gly Ile Ala Ile Thr Ser Met Asp Asp Phe Asn Ser<br>1110 1115 1120      | 720 |
| CAT CCG ATT ACA TTA AAT AAA AAA CAA GTA GAT AAT CTG CTA AAT AAT<br>His Pro Ile Thr Leu Asn Lys Lys Gln Val Asp Asn Leu Leu Asn Asn<br>1125 1130 1135 1140 | 768 |
| AAA CCT ATG ATG TTG GAA ACA AAC CAA ACA GAT GGT GTT TAT AAG ATA<br>Lys Pro Met Met Leu Glu Thr Asn Gln Thr Asp Gly Val Tyr Lys Ile<br>1145 1150 1155      | 816 |
| AAA GAT ACA CAT GGA AAT ATA GTA ACT GGC GGA GAA TGG AAT GGT GTC<br>Lys Asp Thr His Gly Asn Ile Val Thr Gly Gly Glu Trp Asn Gly Val                        | 864 |

- 48 -

| 1160                                                                                                                                                      | 1165 | 1170 |      |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------|------|------|------|
| ATA CAA CAA ATC AAG GCT AAA ACA GCG TCT ATT ATT GTG GAT GAT GGG<br>Ile Gln Gln Ile Lys Ala Lys Thr Ala Ser Ile Ile Val Asp Asp Gly<br>1175 1180 1185      |      |      | 912  |
| GAA CGT GTA GCA GAA AAA CGT GTA GCG GCA AAA GAT TAT GAA AAT CCA<br>Glu Arg Val Ala Glu Lys Arg Val Ala Ala Lys Asp Tyr Glu Asn Pro<br>1190 1195 1200      |      |      | 960  |
| GAA GAT AAA ACA CCG TCT TTA ACT TTA AAA GAT GCC CTG AAG CTT TCA<br>Glu Asp Lys Thr Pro Ser Leu Thr Leu Lys Asp Ala Leu Lys Leu Ser<br>1205 1210 1215 1220 |      |      | 1008 |
| TAT CCA GAT GAA ATA AAA GAA ATA GAG GGA TTA TTA TAT TAT AAA AAC<br>Tyr Pro Asp Glu Ile Lys Glu Ile Glu Gly Leu Leu Tyr Tyr Lys Asn<br>1225 1230 1235      |      |      | 1056 |
| AAA CCG ATA TAC GAA TCG AGC GTT ATG ACT TAC TTA GAT GAA AAT ACA<br>Lys Pro Ile Tyr Glu Ser Ser Val Met Thr Tyr Leu Asp Glu Asn Thr<br>1240 1245 1250      |      |      | 1104 |
| GCA AAA GAA GTG ACC AAA CAA TTA AAT GAT ACC ACT GGG AAA TTT AAA<br>Ala Lys Glu Val Thr Lys Gln Leu Asn Asp Thr Thr Gly Lys Phe Lys<br>1255 1260 1265      |      |      | 1152 |
| GAT GTA AGT CAT TTA TAT GAT GTA AAA CTG ACT CCA AAA ATG AAT GTT<br>Asp Val Ser His Leu Tyr Asp Val Lys Leu Thr Pro Lys Met Asn Val<br>1270 1275 1280      |      |      | 1200 |
| ACA ATC AAA TTG TCT ATA CTT TAT GAT AAT GCT GAG TCT AAT GAT AAC<br>Thr Ile Lys Leu Ser Ile Leu Tyr Asp Asn Ala Glu Ser Asn Asp Asn<br>1285 1290 1295 1300 |      |      | 1248 |
| TCA ATT GGT AAA TGG ACA AAC ACA AAT ATT GTT TCA GGT GGA AAT AAC<br>Ser Ile Gly Lys Trp Thr Asn Thr Asn Ile Val Ser Gly Gly Asn Asn<br>1305 1310 1315      |      |      | 1296 |
| GGA AAA AAA CAA TAT TCT TCT AAT AAT CCG GAT GCT AAT TTG ACA TTA<br>Gly Lys Lys Gln Tyr Ser Ser Asn Asn Pro Asp Ala Asn Leu Thr Leu<br>1320 1325 1330      |      |      | 1344 |
| AAT ACA GAT GCT CAA GAA AAA TTA AAT AAA AAT CGT GAC TAT TAT ATA<br>Asn Thr Asp Ala Gln Glu Lys Leu Asn Lys Asn Arg Asp Tyr Tyr Ile<br>1335 1340 1345      |      |      | 1392 |
| AGT TTA TAT ATG AAG TCA GAA AAA AAC ACA CAA TGT GAG ATT ACT ATA<br>Ser Leu Tyr Met Lys Ser Glu Lys Asn Thr Gln Cys Glu Ile Thr Ile<br>1350 1355 1360      |      |      | 1440 |
| GAT GGG GAG ATT TAT CCG ATC ACT ACA AAA ACA GTG AAT GTG AAT AAA<br>Asp Gly Glu Ile Tyr Pro Ile Thr Thr Lys Thr Val Asn Val Asn Lys<br>1365 1370 1375 1380 |      |      | 1488 |
| GAC AAT TAC AAA AGA TTA GAT ATT ATA GCT CAT AAT ATA AAA AGT AAT                                                                                           |      |      | 1536 |

- 49 -

|                                                                 |      |
|-----------------------------------------------------------------|------|
| Asp Asn Tyr Lys Arg Leu Asp Ile Ile Ala His Asn Ile Lys Ser Asn |      |
| 1385 1390 1395                                                  |      |
| CCA ATT TCT TCA CTT CAT ATT AAA ACG AAT GAT GAA ATA ACT TTA TTT | 1584 |
| Pro Ile Ser Ser Leu His Ile Lys Thr Asn Asp Glu Ile Thr Leu Phe |      |
| 1400 1405 1410                                                  |      |
| TGG GAT GAT ATT TCT ATA ACA GAT GTA GCA TCA ATA AAA CCG GAA AAT | 1632 |
| Trp Asp Asp Ile Ser Ile Thr Asp Val Ala Ser Ile Lys Pro Glu Asn |      |
| 1415 1420 1425                                                  |      |
| TTA ACA GAT TCA GAA ATT AAA CAG ATT TAT AGT AGG TAT GGT ATT AAG | 1680 |
| Leu Thr Asp Ser Glu Ile Lys Gln Ile Tyr Ser Arg Tyr Gly Ile Lys |      |
| 1430 1435 1440                                                  |      |
| TTA GAA GAT GGA ATC CTT ATT GAT AAA AAA GGT GGG ATT CAT TAT GGT | 1728 |
| Leu Glu Asp Gly Ile Leu Ile Asp Lys Lys Gly Gly Ile His Tyr Gly |      |
| 1445 1450 1455 1460                                             |      |
| GAA TTT ATT AAT GAA GCT AGT TTT AAT ATT GAA CCA TTG CCA AAT TAT | 1776 |
| Glu Phe Ile Asn Glu Ala Ser Phe Asn Ile Glu Pro Leu Pro Asn Tyr |      |
| 1465 1470 1475                                                  |      |
| GTG ACC AAA TAT GAA GTT ACT TAT AGT AGT GAG TTA GGA CCA AAC GTG | 1824 |
| Val Thr Lys Tyr Glu Val Thr Tyr Ser Ser Glu Leu Gly Pro Asn Val |      |
| 1480 1485 1490                                                  |      |
| AGT GAC ACA CTT GAA AGT GAT AAA ATT TAC AAG GAT GGG ACA ATT AAA | 1872 |
| Ser Asp Thr Leu Glu Ser Asp Lys Ile Tyr Lys Asp Gly Thr Ile Lys |      |
| 1495 1500 1505                                                  |      |
| TTT GAT TTT ACC AAA TAT AGT AAA AAT GAA CAA GGA TTA TTT TAT GAC | 1920 |
| Phe Asp Phe Thr Lys Tyr Ser Lys Asn Glu Gln Gly Leu Phe Tyr Asp |      |
| 1510 1515 1520                                                  |      |
| AGT GGA TTA AAT TGG GAC TTT AAA ATT AAT GCT ATT ACT TAT GAT GGT | 1968 |
| Ser Gly Leu Asn Trp Asp Phe Lys Ile Asn Ala Ile Thr Tyr Asp Gly |      |
| 1525 1530 1535 1540                                             |      |
| AAA GAG ATG AAT GTT TTT CAT AGA TAT AAT AAA TAG                 | 2004 |
| Lys Glu Met Asn Val Phe His Arg Tyr Asn Lys                     |      |
| 1545 1550                                                       |      |

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

- 50 -

Met Lys Arg Glu Ile Asp Glu Asp Thr Asp Thr Asp Gly Asp Ser Ile  
 1 5 10 15  
 Pro Asp Leu Trp Glu Glu Asn Gly Tyr Thr Ile Gln Asn Arg Ile Ala  
 20 25 30  
 Val Lys Trp Asp Asp Ser Leu Ala Ser Lys Gly Tyr Thr Lys Phe Val  
 35 40 45  
 Ser Asn Pro Leu Glu Ser His Thr Val Gly Asp Pro Tyr Thr Asp Tyr  
 50 55 60  
 Glu Lys Ala Ala Arg Asp Leu Asp Leu Ser Asn Ala Lys Glu Thr Phe  
 65 70 75 80  
 Asn Pro Leu Val Ala Ala Phe Pro Ser Val Asn Val Ser Met Glu Lys  
 85 90 95  
 Val Ile Leu Ser Pro Asn Glu Asn Leu Ser Asn Ser Val Glu Ser His  
 100 105 110  
 Ser Ser Thr Asn Trp Ser Tyr Thr Asn Thr Glu Gly Ala Ser Val Glu  
 115 120 125  
 Ala Gly Ile Gly Pro Lys Gly Ile Ser Phe Gly Val Ser Val Asn Tyr  
 130 135 140  
 Gln His Ser Glu Thr Val Ala Gln Glu Trp Gly Thr Ser Thr Gly Asn  
 145 150 155 160  
 Thr Ser Gln Phe Asn Thr Ala Ser Ala Gly Tyr Leu Asn Ala Asn Val  
 165 170 175  
 Arg Tyr Asn Asn Val Gly Thr Gly Ala Ile Tyr Asp Val Lys Pro Thr  
 180 185 190  
 Thr Ser Phe Val Leu Asn Asn Asp Thr Ile Ala Thr Ile Thr Ala Lys  
 195 200 205  
 Ser Asn Ser Thr Ala Leu Asn Ile Ser Pro Gly Glu Ser Tyr Pro Lys  
 210 215 220  
 Lys Gly Gln Asn Gly Ile Ala Ile Thr Ser Met Asp Asp Phe Asn Ser  
 225 230 235 240  
 His Pro Ile Thr Leu Asn Lys Lys Gln Val Asp Asn Leu Leu Asn Asn  
 245 250 255  
 Lys Pro Met Met Leu Glu Thr Asn Gln Thr Asp Gly Val Tyr Lys Ile  
 260 265 270  
 Lys Asp Thr His Gly Asn Ile Val Thr Gly Gly Glu Trp Asn Gly Val  
 275 280 285  
 Ile Gln Gln Ile Lys Ala Lys Thr Ala Ser Ile Ile Val Asp Asp Gly



|                     |                                             |                             |
|---------------------|---------------------------------------------|-----------------------------|
| 290                 | 295                                         | 300                         |
| Glu Arg Val Ala Glu | Lys Arg Val Ala Ala                         | Lys Asp Tyr Glu Asn Pro     |
| 305                 | 310                                         | 315 320                     |
| Glu Asp Lys Thr Pro | Ser Leu Thr Leu                             | Lys Asp Ala Leu Lys Leu Ser |
|                     | 325                                         | 330 335                     |
| Tyr Pro Asp Glu Ile | Lys Glu Ile Glu Gly Leu Leu Tyr Tyr Lys Asn |                             |
|                     | 340                                         | 345 350                     |
| Lys Pro Ile Tyr Glu | Ser Ser Val Met Thr Tyr Leu Asp Glu Asn Thr |                             |
|                     | 355                                         | 360 365                     |
| Ala Lys Glu Val Thr | Lys Gln Leu Asn Asp Thr Thr Gly Lys Phe Lys |                             |
|                     | 370                                         | 375 380                     |
| Asp Val Ser His Leu | Tyr Asp Val Lys Leu Thr Pro Lys Met Asn Val |                             |
|                     | 385                                         | 390 395 400                 |
| Thr Ile Lys Leu Ser | Ile Leu Tyr Asp Asn Ala Glu Ser Asn Asp Asn |                             |
|                     | 405                                         | 410 415                     |
| Ser Ile Gly Lys Trp | Thr Asn Thr Asn Ile Val Ser Gly Gly Asn Asn |                             |
|                     | 420                                         | 425 430                     |
| Gly Lys Lys Gln Tyr | Ser Ser Asn Asn Pro Asp Ala Asn Leu Thr Leu |                             |
|                     | 435                                         | 440 445                     |
| Asn Thr Asp Ala Gln | Glu Lys Leu Asn Lys Asn Arg Asp Tyr Tyr Ile |                             |
|                     | 450                                         | 455 460                     |
| Ser Leu Tyr Met Lys | Ser Glu Lys Asn Thr Gln Cys Glu Ile Thr Ile |                             |
|                     | 465                                         | 470 475 480                 |
| Asp Gly Glu Ile Tyr | Pro Ile Thr Thr Lys Thr Val Asn Val Asn Lys |                             |
|                     | 485                                         | 490 495                     |
| Asp Asn Tyr Lys Arg | Leu Asp Ile Ile Ala His Asn Ile Lys Ser Asn |                             |
|                     | 500                                         | 505 510                     |
| Pro Ile Ser Ser Leu | His Ile Lys Thr Asn Asp Glu Ile Thr Leu Phe |                             |
|                     | 515                                         | 520 525                     |
| Trp Asp Asp Ile Ser | Ile Thr Asp Val Ala Ser Ile Lys Pro Glu Asn |                             |
|                     | 530                                         | 535 540                     |
| Leu Thr Asp Ser Glu | Ile Lys Gln Ile Tyr Ser Arg Tyr Gly Ile Lys |                             |
|                     | 545                                         | 550 555 560                 |
| Leu Glu Asp Gly Ile | Leu Ile Asp Lys Lys Gly Gly Ile His Tyr Gly |                             |
|                     | 565                                         | 570 575                     |
| Glu Phe Ile Asn Glu | Ala Ser Phe Asn Ile Glu Pro Leu Pro Asn Tyr |                             |
|                     | 580                                         | 585 590                     |

- 52 -

Val Thr Lys Tyr Glu Val Thr Tyr Ser Ser Glu Leu Gly Pro Asn Val  
 595 600 605

Ser Asp Thr Leu Glu Ser Asp Lys Ile Tyr Lys Asp Gly Thr Ile Lys  
 610 615 620

Phe Asp Phe Thr Lys Tyr Ser Lys Asn Glu Gln Gly Leu Phe Tyr Asp  
 625 630 635 640

Ser Gly Leu Asn Trp Asp Phe Lys Ile Asn Ala Ile Thr Tyr Asp Gly  
 645 650 655

Lys Glu Met Asn Val Phe His Arg Tyr Asn Lys  
 660 665

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (iii) HYPOTHETICAL: NO

## (v) FRAGMENT TYPE: N-terminal

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Bacillus cereus
- (B) STRAIN: AB78
- (C) INDIVIDUAL ISOLATE: NRRL B-21058

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "N-terminal sequence of protein purified from strain AB78"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Lys Arg Glu Ile Asp Glu Asp Thr Asp Thr Asx Gly Asp Ser Ile Pro  
 1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- 53 -

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..21

(D) OTHER INFORMATION: /note= "Oligonucleotide probe based  
on amino acids 3 to 9 of SEQ ID NO:8, using codon usage of  
Bacillus thuringiensis"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAAATTGATC AAGATACNGA T

21

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Bacillus thuringiensis

(B) STRAIN: AB88

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..14

(D) OTHER INFORMATION: /note= "N-terminal amino acid  
sequence of protein known as anion exchange fraction 23  
(smaller)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Glu | Pro | Phe | Val | Ser | Ala | Xaa | Xaa | Xaa | Gln | Xaa | Xaa | Xaa |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Xaa Glu Tyr Glu Asn Val Glu Pro Phe Val Ser Ala Xaa  
— 1 5 10

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Asn Lys Asn Asn Thr Lys Leu Pro Thr Arg Ala Leu Pro  
1 5 10

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*  
(B) STRAIN: AB88

(ix) **FEATURE:**

(A) NAME/KEY: Peptide  
(B) LOCATION: 1..15

- 55 -

(D) OTHER INFORMATION: /note= "N-terminal amino acid sequence of 35 kDa VIP active against Agrotis ipsilon"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Leu | Ser | Glu | Asn | Thr | Gly | Lys | Asp | Gly | Gly | Tyr | Ile | Val | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Bacillus thuringiensis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

|     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Asn | Asn | Pro | Asn | Ile | Asn | Glu |
| 1   |     |     |     | 5   |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..9
- (D) OTHER INFORMATION: /note= "N-terminal sequence of 80 kDa delta-endotoxin"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

|     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Asn | Asn | Pro | Asn | Ile | Asn | Glu |
| 1   |     |     |     | 5   |     |     |     |     |

- 56 -

## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Bacillus thuringiensis*
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..11
  - (D) OTHER INFORMATION: /note= "N-terminal sequence from 60 kDa delta-endotoxin"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Val | Leu | Asn | Ser | Gly | Arg | Thr | Thr | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

## (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2655 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..2652
  - (D) OTHER INFORMATION: /note= "Maize optimized DNA sequence for 100 kd VIP1A(a) protein from AB78"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGAAGAACA TGAAGAAGAA GCTGGCCAGC GTGGTGACCT GCACCCCTGCT GGCCCCCATG

|                                                                   |      |
|-------------------------------------------------------------------|------|
| TTCTTGAACG GCAACGTGAA CGCCGTGTAC GCCGACAGCA AGACCAACCA GATCAGCACC | 120  |
| ACCCAGAAGA ACCAGCAGAA GGAGATGGAC CGCAAGGGCC TGCTGGGCTA CTACTTCAAG | 180  |
| GGCAAGGACT TCAGCAACCT GACCATGTTC GCCCCACGC GTGACAGCAC CCTGATCTAC  | 240  |
| GACCAGCAGA CCGCCAACAA GCTGCTGGAC AAGAAGCAGC AGGAGTACCA GAGCATCCGC | 300  |
| TGGATCGGCC TGATCCAGAG CAAGGAGACC GGCGACTTCA CCTTCAACCT GAGCGAGGAC | 360  |
| GAGCAGGCCA TCATCGAGAT CAACGGCAAG ATCATCAGCA ACAAGGGCAA GGAGAAGCAG | 420  |
| GTGGTGCACC TGGAGAAGGG CAAGCTGGTG CCCATCAAGA TCGAGTACCA GAGCGACACC | 480  |
| AAGTTCAACA TCGACAGCAA GACCTTCAAG GAGCTGAAGC TTTTCAAGAT CGACAGCCAG | 540  |
| AACCAGCCCC AGCAGGTGCA GCAGGACGAG CTGCGCAACC CCGAGTTCAA CAAGAAGGAG | 600  |
| AGCCAGGAGT TCCTGGCCAA GCCAGCAAG ATCAACCTGT TCACCCAGCA GATGAAGCGC  | 660  |
| GAGATCGACG AGGACACCGA CACCGACGGC GACAGCATCC CCGACCTGTG GGAGGAGAAC | 720  |
| GGCTACACCA TCCAGAACCG CATCGCCGTG AAGTGGGACG ACAGCCTGGC TAGCAAGGGC | 780  |
| TACACCAAGT TCGTGAGCAA CCCCCTGGAG AGCCACACCG TGGGCGACCC CTACACCGAC | 840  |
| TACGAGAAGG CCGCCCCCGA CCTGGACCTG AGCAACGCCA AGGAGACCTT CAACCCCCTG | 900  |
| GTGGCCGCCT TCCCAGCGT GAACGTGAGC ATGGAGAAGG TGATCCTGAG CCCCACGAG   | 960  |
| AACCTGAGCA ACAGCGTGA GAGCCACTCG AGCACCAACT GGAGCTACAC CAACACCGAG  | 1020 |
| GGCGCCAGCG TGGAGGCCGG CATCGGTCCC AAGGGCATCA GCTTCGGCGT GAGCGTGAAC | 1080 |
| TACCAGCACA GCGAGACCGT GGCCAGGAG TGGGGCACCA GCACCGGCAA CACCAGCCAG  | 1140 |
| TTCAACACCG CCAGCGCCGG CTACCTGAAC GCCAACGTGC GCTACAACAA CGTGGGCACC | 1200 |
| GGCGCCATCT ACGACGTGAA GCCCACCACC AGCTTCGTGC TGAACAACGA CACCATCGCC | 1260 |
| ACCATCACCG CCAAGTCGAA TTCCACCGCC CTGAACATCA GCCCCGGGA GAGCTACCCC  | 1320 |
| AAGAAGGGCC AGAACGGCAT CGCCATCACC AGCATGGACG ACTTCAACAG CCACCCCATC | 1380 |
| ACCCTGAACA AGAAGCAGGT GGACAACCTG CTGAACAACA AGCCCATGAT GCTGGAGACC | 1440 |
| AACCAGACCG ACGGCGTCTA CAAGATCAAG GACACCCACG GCAACATCGT GACCGGGCGC | 1500 |
| GAGTGAACG GCGTGATCCA GCAGATCAAG GCCAAGACCG CCAGCATCAT CGTCGACGAC  | 1560 |
| GGCGAGCGCG TGGCCGAGAA GCGCGTGGCC GCCAAGGACT ACGAGAACCC CGAGGACAAG | 1620 |
| ACCCCCAGCC TGACCCTGAA GGACGCCCTG AAGCTGAGCT ACCCCGACGA GATCAAGGAG | 1680 |
| ATCGAGGGCC TGCTGTACTA CAAGAACAAG CCCATCTACG AGAGCAGCGT GATGACCTAT | 1740 |

- 58 -

|                                                                   |      |
|-------------------------------------------------------------------|------|
| CTAGACGAGA ACACCGCCAA GGAGGTGACC AAGCAGCTGA ACGACACCAC CGGCAAGTTC | 1800 |
| AAGGACGTGA GCCACCTGTA CGACGTGAAG CTGACCCCA AGATGAACGT GACCATCAAG  | 1860 |
| CTGAGCATCC TGTACGACAA CGCCGAGAGC AACGACAACA GCATCGGCAA GTGGACCAAC | 1920 |
| ACCAACATCG TGAGCGGCGG CAACAACGGC AAGAAGCAGT ACAGCAGCAA CAACCCGAG  | 1980 |
| GCCAACTGA CCTGAACAC CGACGCCAG GAGAAGCTGA ACAAGAACCG CGACTACTAC    | 2040 |
| ATCAGCCTGT ACATGAAGAG CGAGAAGAAC ACCCAGTGG AGATCACCAT CGAGGGCGAG  | 2100 |
| ATATACCCCA TCACCACCAA GACCGTGAAC GTGAACAAGG ACAACTACAA GCGCCTGGAC | 2160 |
| ATCATGCCCC ACAACATCAA GAGCAACCCC ATCAGCAGCC TGCACATCAA GACCAACGAC | 2220 |
| GAGATCAGCC TGTCTGGGA CGACATATCG ATTACGACG TOGCCAGCAT CAAGCCCGAG   | 2280 |
| AACCTGACCG ACAGCGAGAT CAAGCAGATA TACAGTCGCT ACGGCATCAA GCTGGAGGAC | 2340 |
| GGCATCTGA TCGACAAGAA GGGCGGCATC CACTACGGCG AGTTCATCAA CGAGGCCAGC  | 2400 |
| TTCAACATCG AGCCCCTGCA GAACTACGTG ACCAAGTACG AGGTGACCTA CAGCAGCGAG | 2460 |
| CTGGGCCCCA ACGTGAGCGA CACCCTGGAG AGCGACAAGA TTTACAAGGA CGGCACCATC | 2520 |
| AAGTTCGACT TCACCAAGTA CAGCAAGAAC GAGCAGGGCC TGTCTACGA CAGCGGCTG   | 2580 |
| AACTGGGACT TCAAGATCAA CGCCATCACC TACGACGGCA AGGAGATGAA CGTGTTCAC  | 2640 |
| CGCTACAACA AGTAG                                                  | 2655 |

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2004 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..2004
- (D) OTHER INFORMATION: /note= "Maize optimized DNA sequence for VIPLA(a) 80 kd protein from AB78"



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ATGAAGCGCG AGATGACGA GGACACCGAC ACCGACGGCG ACAGCATCCC CGACCTGTGG   | 60   |
| GAGGAGAACG GCTACACCAT CCAGAACCGC ATCGCCGTGA AGTGGGACGA CAGCCTGGCT  | 120  |
| AGCAAGGGCT ACACCAAGTT CGTGAGCAAC CCCCTGGAGA GCCACACCGT GGGCGACCCC  | 180  |
| TACACCGACT ACGAGAAGGC CGCCCGGAC CTGGACCTGA GCAACGCCAA GGAGACCTTC   | 240  |
| AACCCCTGG TGGCGCCTT CCCAGCGTG AACGTGAGCA TGGAGAAGGT GATCCTGAGC     | 300  |
| CCCAACGAGA ACCTGAGCAA CAGCGTGGAG AGCCACTCGA GCACCAACTG GAGTACACC   | 360  |
| AACACCGAGG GCGCCAGCGT GGAGGCCGGC ATCGGTCCCA AGGGCATCAG CTTCGGCGTG  | 420  |
| AGCGTGAACT ACCAGCACAG CGAGACCGTG GCCAGGAGT GGGGCACCAG CACCGGCAAC   | 480  |
| ACCAGCCAGT TCAACACCGC CAGCGCCGGC TACCTGAACG CCAACGTGGG CTACAACAAC  | 540  |
| GTGGGCACCG GCGCCATCTA CGACGTGAAG CCCACCACCA GCTTGTGCT GAACAACGAC   | 600  |
| ACCATCGCCA CCATCACCGC CAAGTGAAT TCCACGCCC TGAACATCAG CCCCGGCGAG    | 660  |
| AGCTACCCCA AGAAGGGCCA GAAAGGCATC GCCATCACCA GCATGGACGA CTTCAACAGC  | 720  |
| CACCCCATCA CCTGAACAA GAAGCAGGTG GACAACCTGC TGAACAACAA GCCATGATG    | 780  |
| CTGGAGACCA ACCAGACCGA CGCGTCTAC AAGATCAAGG ACACCCACGG CAACATCGTG   | 840  |
| ACCGGCGGCG AGTGAACCG CGTGATCCAG CAGATCAAGG CCAAGACCGC CAGCATCATC   | 900  |
| GTCGACGACG GCGAGCGCGT GGCGAGAAG CGCGTGGCG CCAAGGACTA CGAGAACCCC    | 960  |
| GAGGACAAGA CCCCAGCCT GACCTGAAG GACGCCCTGA AGCTGAGCTA CCCCAGCGAG    | 1020 |
| ATCAAGGAGA TCGAGGCGCT GCTGTACTAC AAGAACAAGC CCATCTACGA GAGCAGCGTG  | 1080 |
| ATGACCTATC TAGACGAGAA CACCGCCAAG GAGGTGACCA AGCAGCTGAA CGACACCACC  | 1140 |
| GGCAAGTTCA AGGACGTGAG CCACCTGTAC GACGTGAAGC TGACCCCAA GATGAACGTG   | 1200 |
| ACCATCAAGC TGAGCATCCT GTACGACAAC GCCGAGAGCA ACGACAACAG CATCGGCAAG  | 1260 |
| TGGACCAACA CCAACATCGT GAGCGGCGGC AACAAACGCA AGAAGCAGTA CAGCAGCAAC  | 1320 |
| AACCCCGACG CCAACCTGAC CCTGAACACC GACGCCAGG AGAAGCTGAA CAAGAACCGC   | 1380 |
| GACTIONTACA TCAGCCTGTA CATGAAGAGC GAGAAGAACA CCCAGTGGCA GATCACCATC | 1440 |
| GACGGCGAGA TATACCCCAT CACCACCAAG ACCGTGAACG TGAACAAGGA CAACTACAAG  | 1500 |
| CGCCTGGACA TCATCGCCA CAACATCAAG AGCAACCCCA TCAGCAGCCT GCACATCAAG   | 1560 |
| ACCAACGACG AGATCACCTT GTTCTGGGAC GACATATCGA TTACCGACGT CGCCAGCATC  | 1620 |

- 60 -

```

AAGCCCCGAGA ACCTGACCGA CAGCGAGATC AAGCAGATAT ACAGTCGCTA CGGCATCAAG 1680
CTGGAGGACG GCATCCTGAT CGACAAGAAG GGCGGCATCC ACTACGGCGA GTTCATCAAC 1740
GAGGCCAGCT TCAACATCGA GCCCCTGCAG AACTACGTGA CCAAGTACGA GGTGACCTAC 1800
AGCAGCGAGC TGGGCCCCAA CGTGAGCGAC ACCCTGGAGA GCGACAAGAT TTACAAGGAC 1860
GGCACCATCA AGTTCGACTT CACCAAGTAC AGCAAGAACG AGCAGGGCCT GTTCTACGAC 1920
AGCGGCCTGA ACTGGGACTT CAAGATCAAC GCCATCACCT ACGACGGCAA GGAGATGAAC 1980
GTGTTCCACC GCTACAACAA GTAG 2004

```

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1386
- (D) OTHER INFORMATION: /product= "VIP2A(b) from Btt"

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1394..3895
- (D) OTHER INFORMATION: /product= "VIP1A(b) from Btt"

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..4074
- (D) OTHER INFORMATION: /note= "Cloned DNA sequence from Btt which contains the genes for both VIP1A(b) and VIP2A(b) "

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

ATG CAA AGA ATG GAG GGA AAG TTG TTT GTG GTG TCA AAA ACA TTA CAA 48
Met Gln Arg Met Glu Gly Lys Leu Phe Val Val Ser Lys Thr Leu Gln
 670 675 680

GTA GTT ACT AGA ACT GTA TTG CTT AGT ACA GTT TAC TCT ATA ACT TTA 96
Val Val Thr Arg Thr Val Leu Ser Thr Val Tyr Ser Ile Thr Leu
 685 690 695

TTA AAT AAT GTA GTG ATA AAA GCT GAC CAA TTA AAT ATA AAT TCT CAA 144
Leu Asn Asn Val Val Ile Lys Ala Asp Gln Leu Asn Ile Asn Ser Gln

```

- 61 -

|                                                                 |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| 700                                                             | 705 | 710 | 715 |     |
| AGT AAA TAT ACT AAC TTG CAA AAT CTA AAA ATC CCT GAT AAT GCA GAG |     |     |     | 192 |
| Ser Lys Tyr Thr Asn Leu Gln Asn Leu Lys Ile Pro Asp Asn Ala Glu |     |     |     |     |
|                                                                 | 720 | 725 | 730 |     |
| GAT TTT AAA GAA GAT AAG GGG AAA GCG AAA GAA TGG GGG AAA GAG AAA |     |     |     | 240 |
| Asp Phe Lys Glu Asp Lys Gly Lys Ala Lys Glu Trp Gly Lys Glu Lys |     |     |     |     |
|                                                                 | 735 | 740 | 745 |     |
| GGG GAA GAG TGG AGG CCT CCT GCT ACT GAG AAA GGA GAA ATG AAT AAT |     |     |     | 288 |
| Gly Glu Glu Trp Arg Pro Pro Ala Thr Glu Lys Gly Glu Met Asn Asn |     |     |     |     |
|                                                                 | 750 | 755 | 760 |     |
| TTT TTA GAT AAT AAA AAT GAT ATA AAG ACC AAT TAT AAA GAA ATT ACT |     |     |     | 336 |
| Phe Leu Asp Asn Lys Asn Asp Ile Lys Thr Asn Tyr Lys Glu Ile Thr |     |     |     |     |
|                                                                 | 765 | 770 | 775 |     |
| TTT TCT ATG GCA GGT TCA TGT GAA GAT GAA ATA AAA GAT TTA GAA GAA |     |     |     | 384 |
| Phe Ser Met Ala Gly Ser Cys Glu Asp Glu Ile Lys Asp Leu Glu Glu |     |     |     |     |
|                                                                 | 780 | 785 | 790 | 795 |
| ATT GAT AAG ATC TTT GAT AAA GCC AAT CTC TCG AGT TCT ATT ATC ACC |     |     |     | 432 |
| Ile Asp Lys Ile Phe Asp Lys Ala Asn Leu Ser Ser Ser Ile Ile Thr |     |     |     |     |
|                                                                 | 800 | 805 | 810 |     |
| TAT AAA AAT GTG GAA CCA GCA ACA ATT GGA TTT AAT AAA TCT TTA ACA |     |     |     | 480 |
| Tyr Lys Asn Val Glu Pro Ala Thr Ile Gly Phe Asn Lys Ser Leu Thr |     |     |     |     |
|                                                                 | 815 | 820 | 825 |     |
| GAA GGT AAT ACG ATT AAT TCT GAT GCA ATG GCA CAG TTT AAA GAA CAA |     |     |     | 528 |
| Glu Gly Asn Thr Ile Asn Ser Asp Ala Met Ala Gln Phe Lys Glu Gln |     |     |     |     |
|                                                                 | 830 | 835 | 840 |     |
| TTT TTA GGT AAG GAT ATG AAG TTT GAT AGT TAT CTA GAT ACT CAT TTA |     |     |     | 576 |
| Phe Leu Gly Lys Asp Met Lys Phe Asp Ser Tyr Leu Asp Thr His Leu |     |     |     |     |
|                                                                 | 845 | 850 | 855 |     |
| ACT GCT CAA CAA GTT TCC AGT AAA AAA AGA GTT ATT TTG AAG GTT ACG |     |     |     | 624 |
| Thr Ala Gln Gln Val Ser Ser Lys Lys Arg Val Ile Leu Lys Val Thr |     |     |     |     |
|                                                                 | 860 | 865 | 870 | 875 |
| GTT CCG AGT GGG AAA GGT TCT ACT ACT CCA ACA AAA GCA GGT GTC ATT |     |     |     | 672 |
| Val Pro Ser Gly Lys Gly Ser Thr Thr Pro Thr Lys Ala Gly Val Ile |     |     |     |     |
|                                                                 | 880 | 885 | 890 |     |
| TTA AAC AAT AAT GAA TAC AAA ATG CTC ATT GAT AAT GGG TAT GTG CTC |     |     |     | 720 |
| Leu Asn Asn Asn Glu Tyr Lys Met Leu Ile Asp Asn Gly Tyr Val Leu |     |     |     |     |
|                                                                 | 895 | 900 | 905 |     |
| CAT GTA GAT AAG GTA TCA AAA GTA GTA AAA AAA GGG ATG GAG TGC TTA |     |     |     | 768 |
| His Val Asp Lys Val Ser Lys Val Val Lys Lys Gly Met Glu Cys Leu |     |     |     |     |
|                                                                 | 910 | 915 | 920 |     |
| CAA GTT GAA GGG ACT TTA AAA AAG AGT CTC GAC TTT AAA AAT GAT ATA |     |     |     | 816 |

- 62 -

|                                                                 |      |
|-----------------------------------------------------------------|------|
| Gln Val Glu Gly Thr Leu Lys Lys Ser Leu Asp Phe Lys Asn Asp Ile |      |
| 925 930 935                                                     |      |
| AAT GCT GAA GCG CAT AGC TGG GGG ATG AAA ATT TAT GAA GAC TGG GCT | 864  |
| Asn Ala Glu Ala His Ser Trp Gly Met Lys Ile Tyr Glu Asp Trp Ala |      |
| 940 945 950 955                                                 |      |
| AAA AAT TTA ACC GCT TCG CAA AGG GAA GCT TTA GAT GGG TAT GCT AGG | 912  |
| Lys Asn Leu Thr Ala Ser Gln Arg Glu Ala Leu Asp Gly Tyr Ala Arg |      |
| 960 965 970                                                     |      |
| CAA GAT TAT AAA GAA ATC AAT AAT TAT TTG CGC AAT CAA GGC GGG AGT | 960  |
| Gln Asp Tyr Lys Glu Ile Asn Asn Tyr Leu Arg Asn Gln Gly Ser     |      |
| 975 980 985                                                     |      |
| GGA AAT GAA AAG CTG GAT GCC CAA TTA AAA AAT ATT TCT GAT GCT TTA | 1008 |
| Gly Asn Glu Lys Leu Asp Ala Gln Leu Lys Asn Ile Ser Asp Ala Leu |      |
| 990 995 1000                                                    |      |
| GGG AAG AAA CCC ATA CCA GAA AAT ATT ACC GTG TAT AGA TGG TGT GGC | 1056 |
| Gly Lys Lys Pro Ile Pro Glu Asn Ile Thr Val Tyr Arg Trp Cys Gly |      |
| 1005 1010 1015                                                  |      |
| ATG CCG GAA TTT GGT TAT CAA ATT AGT GAT CCG TTA CCT TCT TTA AAA | 1104 |
| Met Pro Glu Phe Gly Tyr Gln Ile Ser Asp Pro Leu Pro Ser Leu Lys |      |
| 1020 1025 1030 1035                                             |      |
| GAT TTT GAA GAA CAA TTT TTA AAT ACA ATT AAA GAA GAC AAA GGG TAT | 1152 |
| Asp Phe Glu Glu Gln Phe Leu Asn Thr Ile Lys Glu Asp Lys Gly Tyr |      |
| 1040 1045 1050                                                  |      |
| ATG AGT ACA AGC TTA TCG AGT GAA CGT CTT GCA GCT TTT GGA TCT AGA | 1200 |
| Met Ser Thr Ser Leu Ser Ser Glu Arg Leu Ala Ala Phe Gly Ser Arg |      |
| 1055 1060 1065                                                  |      |
| AAA ATT ATA TTA CGC TTA CAA GTT CCG AAA GGA AGT ACG GGG GCG TAT | 1248 |
| Lys Ile Ile Leu Arg Leu Gln Val Pro Lys Gly Ser Thr Gly Ala Tyr |      |
| 1070 1075 1080                                                  |      |
| TTA AGT GCC ATT GGT GGA TTT GCA AGT GAA AAA GAG ATC CTA CTT GAT | 1296 |
| Leu Ser Ala Ile Gly Gly Phe Ala Ser Glu Lys Glu Ile Leu Leu Asp |      |
| 1085 1090 1095                                                  |      |
| AAA GAT AGT AAA TAT CAT ATT GAT AAA GCA ACA GAG GTA ATC ATT AAA | 1344 |
| Lys Asp Ser Lys Tyr His Ile Asp Lys Ala Thr Glu Val Ile Ile Lys |      |
| 1100 1105 1110 1115                                             |      |
| GGT GTT AAG CGA TAT GTA GTG GAT GCA ACA TTA TTA ACA AAT         | 1386 |
| Gly Val Lys Arg Tyr Val Val Asp Ala Thr Leu Leu Thr Asn         |      |
| 1120 1125                                                       |      |
| TAAGGAG ATG AAA AAT ATG AAG AAA AAG TTA GCA AGT GTT GTA ACC TGT | 1435 |
| Met Lys Asn Met Lys Lys Lys Leu Ala Ser Val Val Thr Cys         |      |
| 1 5 10                                                          |      |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| ATG TTA TTA GCT CCT ATG TTT TTG AAT GGA AAT GTG AAT GCT GTT AAC<br>Met Leu Leu Ala Pro Met Phe Leu Asn Gly Asn Val Asn Ala Val Asn<br>15 20 25 30     | 1483 |
| GCG GAT AGT AAA ATA AAT CAG ATT TCT ACA ACG CAG GAA AAC CAA CAG<br>Ala Asp Ser Lys Ile Asn Gln Ile Ser Thr Thr Gln Glu Asn Gln Gln<br>35 40 45        | 1531 |
| AAA GAG ATG GAC CGA AAG GGA TTA TTG GGA TAT TAT TTC AAA GGA AAA<br>Lys Glu Met Asp Arg Lys Gly Leu Leu Gly Tyr Tyr Phe Lys Gly Lys<br>50 55 60        | 1579 |
| GAT TTT AAT AAT CTT ACT ATG TTT GCA CCG ACA CGT GAT AAT ACC CTT<br>Asp Phe Asn Asn Leu Thr Met Phe Ala Pro Thr Arg Asp Asn Thr Leu<br>65 70 75        | 1627 |
| ATG TAT GAC CAA CAA ACA GCG AAT GCA TTA TTA GAT AAA AAA CAA CAA<br>Met Tyr Asp Gln Gln Thr Ala Asn Ala Leu Leu Asp Lys Lys Gln Gln<br>80 85 90        | 1675 |
| GAA TAT CAG TCC ATT CGT TGG ATT GGT TTG ATT CAG CGT AAA GAA ACG<br>Glu Tyr Gln Ser Ile Arg Trp Ile Gly Leu Ile Gln Arg Lys Glu Thr<br>95 100 105 110  | 1723 |
| GCG GAT TTC ACA TTT AAC TTA TCA AAG GAT GAA CAG GCA ATT ATA GAA<br>Gly Asp Phe Thr Phe Asn Leu Ser Lys Asp Glu Gln Ala Ile Ile Glu<br>115 120 125     | 1771 |
| ATC GAT GGG AAA ATC ATT TCT AAT AAA GGG AAA GAA AAG CAA GTT GTC<br>Ile Asp Gly Lys Ile Ile Ser Asn Lys Gly Lys Glu Lys Gln Val Val<br>130 135 140     | 1819 |
| CAT TTA GAA AAA GAA AAA TTA GTT CCA ATC AAA ATA GAG TAT CAA TCA<br>His Leu Glu Lys Glu Lys Leu Val Pro Ile Lys Ile Glu Tyr Gln Ser<br>145 150 155     | 1867 |
| GAT ACG AAA TTT AAT ATT GAT AGT AAA ACA TTT AAA GAA CTT AAA TTA<br>Asp Thr Lys Phe Asn Ile Asp Ser Lys Thr Phe Lys Glu Leu Lys Leu<br>160 165 170     | 1915 |
| TTT AAA ATA GAT AGT CAA AAC CAA TCT CAA CAA GTT CAA CTG AGA AAC<br>Phe Lys Ile Asp Ser Gln Asn Gln Ser Gln Gln Val Gln Leu Arg Asn<br>175 180 185 190 | 1963 |
| CCT GAA TTT AAC AAA AAA GAA TCA CAG GAA TTT TTA GCA AAA GCA TCA<br>Pro Glu Phe Asn Lys Lys Glu Ser Gln Glu Phe Leu Ala Lys Ala Ser<br>195 200 205     | 2011 |
| AAA ACA AAC CTT TTT AAG CAA AAA ATG AAA AGA GAT ATT GAT GAA GAT<br>Lys Thr Asn Leu Phe Lys Gln Lys Met Lys Arg Asp Ile Asp Glu Asp<br>210 215 220     | 2059 |
| ACG GAT ACA GAT GGA GAC TCC ATT CCT GAT CTT TGG GAA GAA AAT GGG<br>Thr Asp Thr Asp Gly Asp Ser Ile Pro Asp Leu Trp Glu Glu Asn Gly<br>225 230 235     | 2107 |

- 64 -

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| TAC ACG ATT CAA AAT AAA GTT GCT GTC AAA TGG GAT GAT TCG CTA GCA<br>Tyr Thr Ile Gln Asn Lys Val Ala Val Lys Trp Asp Asp Ser Leu Ala<br>240 245 250     | 2155 |
| AGT AAG GGA TAT ACA AAA TTT GTT TCG AAT CCA TTA GAC AGC CAC ACA<br>Ser Lys Gly Tyr Thr Lys Phe Val Ser Asn Pro Leu Asp Ser His Thr<br>255 260 265 270 | 2203 |
| GTT GGC GAT CCC TAT ACT GAT TAT GAA AAG GCC GCA AGG GAT TTA GAT<br>Val Gly Asp Pro Tyr Thr Asp Tyr Glu Lys Ala Ala Arg Asp Leu Asp<br>275 280 285     | 2251 |
| TTA TCA AAT GCA AAG GAA ACG TTC AAC CCA TTG GTA GCT GCT TTT CCA<br>Leu Ser Asn Ala Lys Glu Thr Phe Asn Pro Leu Val Ala Ala Phe Pro<br>290 295 300     | 2299 |
| AGT GTG AAT GTT AGT ATG GAA AAG GTG ATA TTA TCA CCA AAT GAA AAT<br>Ser Val Asn Val Ser Met Glu Lys Val Ile Leu Ser Pro Asn Glu Asn<br>305 310 315     | 2347 |
| TTA TCC AAT AGT GTA GAG TCT CAT TCA TCC ACG AAT TGG TCT TAT ACG<br>Leu Ser Asn Ser Val Glu Ser His Ser Ser Thr Asn Trp Ser Tyr Thr<br>320 325 330     | 2395 |
| AAT ACA GAA GGA GCT TCC ATT GAA GCT GGT GGC GGT CCA TTA GGC CTT<br>Asn Thr Glu Gly Ala Ser Ile Glu Ala Gly Gly Gly Pro Leu Gly Leu<br>335 340 345 350 | 2443 |
| TCT TTT GGC GTG AGT GTT ACT TAT CAA CAC TCT GAA ACA GTT GCA CAA<br>Ser Phe Gly Val Ser Val Thr Tyr Gln His Ser Glu Thr Val Ala Gln<br>355 360 365     | 2491 |
| GAA TGG GGA ACA TCT ACA GGA AAT ACT TCA CAA TTC AAT ACG GCT TCA<br>Glu Trp Gly Thr Ser Thr Gly Asn Thr Ser Gln Phe Asn Thr Ala Ser<br>370 375 380     | 2539 |
| GCG GGA TAT TTA AAT GCA AAT GTT CCG TAT AAC AAT GTA GGG ACT GGT<br>Ala Gly Tyr Leu Asn Ala Asn Val Arg Tyr Asn Asn Val Gly Thr Gly<br>385 390 395     | 2587 |
| GCC ATC TAT GAT GTA AAA CCT ACA ACA AGT TTT GTA TTA AAT AAC AAT<br>Ala Ile Tyr Asp Val Lys Pro Thr Thr Ser Phe Val Leu Asn Asn Asn<br>400 405 410     | 2635 |
| ACC ATC GCA ACG ATT ACA GCA AAA TCA AAT TCA ACA GCT TTA CGT ATA<br>Thr Ile Ala Thr Ile Thr Ala Lys Ser Asn Ser Thr Ala Leu Arg Ile<br>415 420 425 430 | 2683 |
| TCT CCG GGG GAT AGT TAT CCA GAA ATA GGA GAA AAC GCT ATT GCG ATT<br>Ser Pro Gly Asp Ser Tyr Pro Glu Ile Gly Glu Asn Ala Ile Ala Ile<br>435 440 445     | 2731 |
| ACA TCT ATG GAT GAT TTT AAT TCT CAT CCA ATT ACA TTA AAT AAA CAA<br>Thr Ser Met Asp Asp Phe Asn Ser His Pro Ile Thr Leu Asn Lys Gln<br>2779            |      |

- 65 -

|                                                                 |     |     |      |
|-----------------------------------------------------------------|-----|-----|------|
| 450                                                             | 455 | 460 |      |
| CAG GTA AAT CAA TTG ATA AAT AAT AAG CCA ATT ATG CTA GAG ACA GAC |     |     | 2827 |
| Gln Val Asn Gln Leu Ile Asn Asn Lys Pro Ile Met Leu Glu Thr Asp |     |     |      |
| 465                                                             | 470 | 475 |      |
| CAA ACA GAT GGT GTT TAT AAA ATA AGA GAT ACA CAT GGA AAT ATT GTA |     |     | 2875 |
| Gln Thr Asp Gly Val Tyr Lys Ile Arg Asp Thr His Gly Asn Ile Val |     |     |      |
| 480                                                             | 485 | 490 |      |
| ACT GGT GGA GAA TGG AAT GGT GTA ACA CAA CAA ATT AAA GCA AAA ACA |     |     | 2923 |
| Thr Gly Gly Glu Trp Asn Gly Val Thr Gln Ile Lys Ala Lys Thr     |     |     |      |
| 495                                                             | 500 | 505 | 510  |
| GCG TCT ATT ATT GTG GAT GAC GGG AAA CAG GTA GCA GAA AAA CGT GTG |     |     | 2971 |
| Ala Ser Ile Ile Val Asp Asp Gly Lys Gln Val Ala Glu Lys Arg Val |     |     |      |
| 515                                                             | 520 | 525 |      |
| GCG GCA AAA GAT TAT GGT CAT CCA GAA GAT AAA ACA CCA CCT TTA ACT |     |     | 3019 |
| Ala Ala Lys Asp Tyr Gly His Pro Glu Asp Lys Thr Pro Pro Leu Thr |     |     |      |
| 530                                                             | 535 | 540 |      |
| TTA AAA GAT ACC CTG AAG CTT TCA TAC CCA GAT GAA ATA AAA GAA ACT |     |     | 3067 |
| Leu Lys Asp Thr Leu Lys Leu Ser Tyr Pro Asp Glu Ile Lys Glu Thr |     |     |      |
| 545                                                             | 550 | 555 |      |
| AAT GGA TTG TTG TAC TAT GAT GAC AAA CCA ATC TAT GAA TCG AGT GTC |     |     | 3115 |
| Asn Gly Leu Leu Tyr Tyr Asp Asp Lys Pro Ile Tyr Glu Ser Ser Val |     |     |      |
| 560                                                             | 565 | 570 |      |
| ATG ACT TAT CTG GAT GAA AAT ACG GCA AAA GAA GTC AAA AAA CAA ATA |     |     | 3163 |
| Met Thr Tyr Leu Asp Glu Asn Thr Ala Lys Glu Val Lys Lys Gln Ile |     |     |      |
| 575                                                             | 580 | 585 | 590  |
| AAT GAT ACA ACC GGA AAA TTT AAG GAT GTA AAT CAC TTA TAT GAT GTA |     |     | 3211 |
| Asn Asp Thr Thr Gly Lys Phe Lys Asp Val Asn His Leu Tyr Asp Val |     |     |      |
| 595                                                             | 600 | 605 |      |
| AAA CTG ACT CCA AAA ATG AAT TTT ACG ATT AAA ATG GCT TCC TTG TAT |     |     | 3259 |
| Lys Leu Thr Pro Lys Met Asn Phe Thr Ile Lys Met Ala Ser Leu Tyr |     |     |      |
| 610                                                             | 615 | 620 |      |
| GAT GGG GCT GAA AAT AAT CAT AAC TCT TTA GGA ACC TGG TAT TTA ACA |     |     | 3307 |
| Asp Gly Ala Glu Asn Asn His Asn Ser Leu Gly Thr Trp Tyr Leu Thr |     |     |      |
| 625                                                             | 630 | 635 |      |
| TAT AAT GTT GCT GGT GGA AAT ACT GGG AAG AGA CAA TAT CGT TCA GCT |     |     | 3355 |
| Tyr Asn Val Ala Gly Gly Asn Thr Gly Lys Arg Gln Tyr Arg Ser Ala |     |     |      |
| 640                                                             | 645 | 650 |      |
| CAT TCT TGT GCA CAT GTA GCT CTA TCT TCA GAA GCG AAA AAG AAA CTA |     |     | 3403 |
| His Ser Cys Ala His Val Ala Leu Ser Ser Glu Ala Lys Lys Lys Leu |     |     |      |
| 655                                                             | 660 | 665 | 670  |
| AAT CAA AAT GCG AAT TAC TAT CTT AGC ATG TAT ATG AAG GCT GAT TCT |     |     | 3451 |

- 66 -

|                                                                 |      |
|-----------------------------------------------------------------|------|
| Asn Gln Asn Ala Asn Tyr Tyr Leu Ser Met Tyr Met Lys Ala Asp Ser |      |
| 675 680 685                                                     |      |
| ACT ACG GAA CCT ACA ATA GAA GTA GCT GGG GAA AAA TCT GCA ATA ACA | 3499 |
| Thr Thr Glu Pro Thr Ile Glu Val Ala Gly Glu Lys Ser Ala Ile Thr |      |
| 690 695 700                                                     |      |
| AGT AAA AAA GTA AAA TTA AAT AAT CAA AAT TAT CAA AGA GTT GAT ATT | 3547 |
| Ser Lys Lys Val Lys Leu Asn Asn Gln Asn Tyr Gln Arg Val Asp Ile |      |
| 705 710 715                                                     |      |
| TTA GTG AAA AAT TCT GAA AGA AAT CCA ATG GAT AAA ATA TAT ATA AGA | 3595 |
| Leu Val Lys Asn Ser Glu Arg Asn Pro Met Asp Lys Ile Tyr Ile Arg |      |
| 720 725 730                                                     |      |
| GGA AAT GGC ACG ACA AAT GTT TAT GGG GAT GAT GTT ACT ATC CCA GAG | 3643 |
| Gly Asn Gly Thr Thr Asn Val Tyr Gly Asp Asp Val Thr Ile Pro Glu |      |
| 735 740 745 750                                                 |      |
| GTA TCA GCT ATA AAT CCG GCT AGT CTA TCA GAT GAA GAA ATT CAA GAA | 3691 |
| Val Ser Ala Ile Asn Pro Ala Ser Leu Ser Asp Glu Glu Ile Gln Glu |      |
| 755 760 765                                                     |      |
| ATA TTT AAA GAC TCA ACT ATT GAA TAT GGA AAT CCT AGT TTC GTT GCT | 3739 |
| Ile Phe Lys Asp Ser Thr Ile Glu Tyr Gly Asn Pro Ser Phe Val Ala |      |
| 770 775 780                                                     |      |
| GAT GCC GTA ACA TTT AAA AAT ATA AAA CCT TTA CAA AAT TAT GTA AAG | 3787 |
| Asp Ala Val Thr Phe Lys Asn Ile Lys Pro Leu Gln Asn Tyr Val Lys |      |
| 785 790 795                                                     |      |
| GAA TAT GAA ATA TAT CAT AAA TCT CAT CGA TAT GAA AAG AAA ACG GTC | 3835 |
| Glu Tyr Glu Ile Tyr His Lys Ser His Arg Tyr Glu Lys Lys Thr Val |      |
| 800 805 810                                                     |      |
| TTT GAT ATC ATG GGT GTT CAT TAT GAG TAT AGT ATA GCT AGG GAA CAA | 3883 |
| Phe Asp Ile Met Gly Val His Tyr Glu Tyr Ser Ile Ala Arg Glu Gln |      |
| 815 820 825 830                                                 |      |
| AAG AAA GCC GCA TAATTTTAAA AATAAAACTC GTTAGAGTTT ATTTAGCATG     | 3935 |
| Lys Lys Ala Ala                                                 |      |
| GTATTTTAA GAATAATCAA TATGTTGAAC CGTTTGTAGC TGTTTTGGAA GGAATTCA  | 3995 |
| TTTTATTGG TCTCTAAGT TGATGGGCAT GGGATATGTT CAGCATCCAA GCGTTTNGGG | 4055 |
| GGTTANAAAA TCCAATTTT                                            | 4074 |

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462 amino acids

(B) TYPE: amino acid



- 67 -

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Met Gln Arg Met Glu Gly Lys Leu Phe Val Val Ser Lys Thr Leu Gln
 1 5 10 15

Val Val Thr Arg Thr Val Leu Leu Ser Thr Val Tyr Ser Ile Thr Leu
 20 25 30

Leu Asn Asn Val Val Ile Lys Ala Asp Gln Leu Asn Ile Asn Ser Gln
 35 40 45

Ser Lys Tyr Thr Asn Leu Gln Asn Leu Lys Ile Pro Asp Asn Ala Glu
 50 55 60

Asp Phe Lys Glu Asp Lys Gly Lys Ala Lys Glu Trp Gly Lys Glu Lys
65 70 75 80

Gly Glu Glu Trp Arg Pro Pro Ala Thr Glu Lys Gly Glu Met Asn Asn
 85 90 95

Phe Leu Asp Asn Lys Asn Asp Ile Lys Thr Asn Tyr Lys Glu Ile Thr
 100 105 110

Phe Ser Met Ala Gly Ser Cys Glu Asp Glu Ile Lys Asp Leu Glu Glu
 115 120 125

Ile Asp Lys Ile Phe Asp Lys Ala Asn Leu Ser Ser Ser Ile Ile Thr
 130 135 140

Tyr Lys Asn Val Glu Pro Ala Thr Ile Gly Phe Asn Lys Ser Leu Thr
 145 150 155 160

Glu Gly Asn Thr Ile Asn Ser Asp Ala Met Ala Gln Phe Lys Glu Gln
 165 170 175

Phe Leu Gly Lys Asp Met Lys Phe Asp Ser Tyr Leu Asp Thr His Leu
 180 185 190

Thr Ala Gln Gln Val Ser Ser Lys Lys Arg Val Ile Leu Lys Val Thr
 195 200 205

Val Pro Ser Gly Lys Gly Ser Thr Thr Pro Thr Lys Ala Gly Val Ile
 210 215 220

Leu Asn Asn Asn Glu Tyr Lys Met Leu Ile Asp Asn Gly Tyr Val Leu
 225 230 235 240

His Val Asp Lys Val Ser Lys Val Val Lys Lys Gly Met Glu Cys Leu
 245 250 255

Gln Val Glu Gly Thr Leu Lys Lys Ser Leu Asp Phe Lys Asn Asp Ile

```

260  
Asn Ala Glu Ala His Ser Trp Gly Met Lys Ile Tyr Glu Asp Trp Ala  
275 280 285

Lys Asn Leu Thr Ala Ser Gln Arg Glu Ala Leu Asp Gly Tyr Ala Arg  
290 295 300

Gln Asp Tyr Lys Glu Ile Asn Asn Tyr Leu Arg Asn Gln Gly Gly Ser  
305 310 315 320

Gly Asn Glu Lys Leu Asp Ala Gln Leu Lys Asn Ile Ser Asp Ala Leu  
325 330 335

Gly Lys Lys Pro Ile Pro Glu Asn Ile Thr Val Tyr Arg Trp Cys Gly  
340 345 350

Met Pro Glu Phe Gly Tyr Gln Ile Ser Asp Pro Leu Pro Ser Leu Lys  
355 360 365

Asp Phe Glu Glu Gln Phe Leu Asn Thr Ile Lys Glu Asp Lys Gly Tyr  
370 375 380

Met Ser Thr Ser Leu Ser Ser Glu Arg Leu Ala Phe Gly Ser Arg  
385 390 395 400

Lys Ile Ile Leu Arg Leu Gln Val Pro Lys Gly Ser Thr Gly Ala Tyr  
405 410 415

Leu Ser Ala Ile Gly Gly Phe Ala Ser Glu Lys Glu Ile Leu Leu Asp  
420 425 430

Lys Asp Ser Lys Tyr His Ile Asp Lys Ala Thr Glu Val Ile Ile Lys  
435 440 445

Gly Val Lys Arg Tyr Val Val Asp Ala Thr Leu Leu Thr Asn  
450 455 460

(2) INFORMATION FOR SEQ ID NO:21:

(i). SEQUENCE CHARACTERISTICS:

- PROTEIN CHARACTERISTICS:
- (A) LENGTH: 834 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Lys Asn Met Lys Lys Lys Leu Ala Ser Val Val Thr Cys Met Leu  
1 5 10 15  
Leu Ala Pro Met Phe Leu Asn Gly Asn Val Asn Ala Val Asn Ala Asp  
20 25 30

- 69 -

Ser Lys Ile Asn Gln Ile Ser Thr Thr Gln Glu Asn Gln Gln Lys Glu  
 35 40 45  
 Met Asp Arg Lys Gly Leu Leu Gly Tyr Tyr Phe Lys Gly Lys Asp Phe  
 50 55 60  
 Asn Asn Leu Thr Met Phe Ala Pro Thr Arg Asp Asn Thr Leu Met Tyr  
 65 70 75 80  
 Asp Gln Gln Thr Ala Asn Ala Leu Leu Asp Lys Lys Gln Gln Glu Tyr  
 85 90 95  
 Gln Ser Ile Arg Trp Ile Gly Leu Ile Gln Arg Lys Glu Thr Gly Asp  
 100 105 110  
 Phe Thr Phe Asn Leu Ser Lys Asp Glu Gln Ala Ile Ile Glu Ile Asp  
 115 120 125  
 Gly Lys Ile Ile Ser Asn Lys Gly Lys Glu Lys Gln Val Val His Leu  
 130 135 140  
 Glu Lys Glu Lys Leu Val Pro Ile Lys Ile Glu Tyr Gln Ser Asp Thr  
 145 150 155 160  
 Lys Phe Asn Ile Asp Ser Lys Thr Phe Lys Glu Leu Lys Leu Phe Lys  
 165 170 175  
 Ile Asp Ser Gln Asn Gln Ser Gln Gln Val Gln Leu Arg Asn Pro Glu  
 180 185 190  
 Phe Asn Lys Lys Glu Ser Gln Glu Phe Leu Ala Lys Ala Ser Lys Thr  
 195 200 205  
 Asn Leu Phe Lys Gln Lys Met Lys Arg Asp Ile Asp Glu Asp Thr Asp  
 210 215 220  
 Thr Asp Gly Asp Ser Ile Pro Asp Leu Trp Glu Glu Asn Gly Tyr Thr  
 225 230 235 240  
 Ile Gln Asn Lys Val Ala Val Lys Trp Asp Asp Ser Leu Ala Ser Lys  
 245 250 255  
 Gly Tyr Thr Lys Phe Val Ser Asn Pro Leu Asp Ser His Thr Val Gly  
 260 265 270  
 Asp Pro Tyr Thr Asp Tyr Glu Lys Ala Ala Arg Asp Leu Asp Leu Ser  
 275 280 285  
 Asn Ala Lys Glu Thr Phe Asn Pro Leu Val Ala Ala Phe Pro Ser Val  
 290 295 300  
 Asn Val Ser Met Glu Lys Val Ile Leu Ser Pro Asn Glu Asn Leu Ser  
 305 310 315 320

- 70 -

Asn Ser Val Glu Ser His Ser Ser Thr Asn Trp Ser Tyr Thr Asn Thr  
 325 330 335  
 Glu Gly Ala Ser Ile Glu Ala Gly Gly Gly Pro Leu Gly Leu Ser Phe  
 340 345 350  
 Gly Val Ser Val Thr Tyr Gln His Ser Glu Thr Val Ala Gln Glu Trp  
 355 360 365  
 Gly Thr Ser Thr Gly Asn Thr Ser Gln Phe Asn Thr Ala Ser Ala Gly  
 370 375 380  
 Tyr Leu Asn Ala Asn Val Arg Tyr Asn Asn Val Gly Thr Gly Ala Ile  
 385 390 395 400  
 Tyr Asp Val Lys Pro Thr Thr Ser Phe Val Leu Asn Asn Asn Thr Ile  
 405 410 415  
 Ala Thr Ile Thr Ala Lys Ser Asn Ser Thr Ala Leu Arg Ile Ser Pro  
 420 425 430  
 Gly Asp Ser Tyr Pro Glu Ile Gly Glu Asn Ala Ile Ala Ile Thr Ser  
 435 440 445  
 Met Asp Asp Phe Asn Ser His Pro Ile Thr Leu Asn Lys Gln Gln Val  
 450 455 460  
 Asn Gln Leu Ile Asn Asn Lys Pro Ile Met Leu Glu Thr Asp Gln Thr  
 465 470 475 480  
 Asp Gly Val Tyr Lys Ile Arg Asp Thr His Gly Asn Ile Val Thr Gly  
 485 490 495  
 Gly Glu Trp Asn Gly Val Thr Gln Gln Ile Lys Ala Lys Thr Ala Ser  
 500 505 510  
 Ile Ile Val Asp Asp Gly Lys Gln Val Ala Glu Lys Arg Val Ala Ala  
 515 520 525  
 Lys Asp Tyr Gly His Pro Glu Asp Lys Thr Pro Pro Leu Thr Leu Lys  
 530 535 540  
 Asp Thr Leu Lys Leu Ser Tyr Pro Asp Glu Ile Lys Glu Thr Asn Gly  
 545 550 555 560  
 Leu Leu Tyr Tyr Asp Asp Lys Pro Ile Tyr Glu Ser Ser Val Met Thr  
 565 570 575  
 Tyr Leu Asp Glu Asn Thr Ala Lys Glu Val Lys Lys Gln Ile Asn Asp  
 580 585 590  
 Thr Thr Gly Lys Phe Lys Asp Val Asn His Leu Tyr Asp Val Lys Leu  
 595 600 605  
 Thr Pro Lys Met Asn Phe Thr Ile Lys Met Ala Ser Leu Tyr Asp Gly

- 71 -

|                                                                 |     |             |
|-----------------------------------------------------------------|-----|-------------|
| 610                                                             | 615 | 620         |
| Ala Glu Asn Asn His Asn Ser Leu Gly Thr Trp Tyr Leu Thr Tyr Asn |     |             |
| 625                                                             | 630 | 635 640     |
| Val Ala Gly Gly Asn Thr Gly Lys Arg Gln Tyr Arg Ser Ala His Ser |     |             |
|                                                                 | 645 | 650 655     |
| Cys Ala His Val Ala Leu Ser Ser Glu Ala Lys Lys Lys Leu Asn Gln |     |             |
|                                                                 | 660 | 665 670     |
| Asn Ala Asn Tyr Tyr Leu Ser Met Tyr Met Lys Ala Asp Ser Thr Thr |     |             |
|                                                                 | 675 | 680 685     |
| Glu Pro Thr Ile Glu Val Ala Gly Glu Lys Ser Ala Ile Thr Ser Lys |     |             |
|                                                                 | 690 | 695 700     |
| Lys Val Lys Leu Asn Asn Gln Asn Tyr Gln Arg Val Asp Ile Leu Val |     |             |
|                                                                 | 705 | 710 715 720 |
| Lys Asn Ser Glu Arg Asn Pro Met Asp Lys Ile Tyr Ile Arg Gly Asn |     |             |
|                                                                 | 725 | 730 735     |
| Gly Thr Thr Asn Val Tyr Gly Asp Asp Val Thr Ile Pro Glu Val Ser |     |             |
|                                                                 | 740 | 745 750     |
| Ala Ile Asn Pro Ala Ser Leu Ser Asp Glu Glu Ile Gln Glu Ile Phe |     |             |
|                                                                 | 755 | 760 765     |
| Lys Asp Ser Thr Ile Glu Tyr Gly Asn Pro Ser Phe Val Ala Asp Ala |     |             |
|                                                                 | 770 | 775 780     |
| Val Thr Phe Lys Asn Ile Lys Pro Leu Gln Asn Tyr Val Lys Glu Tyr |     |             |
|                                                                 | 785 | 790 795 800 |
| Glu Ile Tyr His Lys Ser His Arg Tyr Glu Lys Lys Thr Val Phe Asp |     |             |
|                                                                 | 805 | 810 815     |
| Ile Met Gly Val His Tyr Glu Tyr Ser Ile Ala Arg Glu Gln Lys Lys |     |             |
|                                                                 | 820 | 825 830     |
| Ala Ala                                                         |     |             |

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4041 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

- 72 -

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..4038

(D) OTHER INFORMATION: /product= "VIP1A(a)/VIP2A(a) fusion product"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

|                                                                                                                                                          |     |
|----------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| ATG AAA AGA ATG GAG GGA AAG TTG TTT ATG GTG TCA AAA AAA TTA CAA<br>Met Lys Arg Met Glu Gly Lys Leu Phe Met Val Ser Lys Lys Leu Gln<br>835 840 845 850    | 48  |
| GTA GTT ACT AAA ACT GTA TTG CTT AGT ACA GTT TTC TCT ATA TCT TTA<br>Val Val Thr Lys Thr Val Leu Leu Ser Thr Val Phe Ser Ile Ser Leu<br>855 860 865        | 96  |
| TTA AAT AAT GAA GTG ATA AAA GCT GAA CAA TTA AAT ATA AAT TCT CAA<br>Leu Asn Asn Glu Val Ile Lys Ala Glu Gln Leu Asn Ile Asn Ser Gln<br>870 875 880        | 144 |
| AGT AAA TAT ACT AAC TTG CAA AAT CTA AAA ATC ACT GAC AAG GTA GAG<br>Ser Lys Tyr Thr Asn Leu Gln Asn Leu Lys Ile Thr Asp Lys Val Glu<br>885 890 895        | 192 |
| GAT TTT AAA GAA GAT AAG GAA AAA GCG AAA GAA TGG GGG AAA GAA AAA<br>Asp Phe Lys Glu Asp Lys Glu Lys Ala Lys Glu Trp Gly Lys Glu Lys<br>900 905 910        | 240 |
| GAA AAA GAG TGG AAA CTA ACT GCT ACT GAA AAA GGA AAA ATG AAT AAT<br>Glu Lys Glu Trp Lys Leu Thr Ala Thr Glu Lys Gly Lys Met Asn Asn<br>915 920 925 930    | 288 |
| TTT TTA GAT AAT AAA AAT GAT ATA AAG ACA AAT TAT AAA GAA ATT ACT<br>Phe Leu Asp Asn Lys Asn Asp Ile Lys Thr Asn Tyr Lys Glu Ile Thr<br>935 940 945        | 336 |
| TTT TCT ATG GCA GGC TCA TTT GAA GAT GAA ATA AAA GAT TTA AAA GAA<br>Phe Ser Met Ala Gly Ser Phe Glu Asp Glu Ile Lys Asp Leu Lys Glu<br>950 955 960        | 384 |
| ATT GAT AAG ATG TTT GAT AAA ACC AAT CTA TCA AAT TCT ATT ATC ACC<br>Ile Asp Lys Met Phe Asp Lys Thr Asn Leu Ser Asn Ser Ile Ile Thr<br>965 970 975        | 432 |
| TAT AAA AAT GTG GAA CCG ACA ACA ATT GGA TTT AAT AAA TCT TTA ACA<br>Tyr Lys Asn Val Glu Pro Thr Thr Ile Gly Phe Asn Lys Ser Leu Thr<br>980 985 990        | 480 |
| GAA GGT AAT ACG ATT AAT TCT GAT GCA ATG GCA CAG TTT AAA GAA CAA<br>Glu Gly Asn Thr Ile Asn Ser Asp Ala Met Ala Gln Phe Lys Glu Gln<br>995 1000 1005 1010 | 528 |
| TTT TTA GAT AGG GAT ATT AAG TTT GAT AGT TAT CTA GAT ACG CAT TTA<br>Phe Leu Asp Arg Asp Ile Lys Phe Asp Ser Tyr Leu Asp Thr His Leu                       | 576 |

- 73 -

| 1015                                                                                                                                                                       | 1020 | 1025 |      |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|------|------|
| ACT GCT CAA CAA GTT TCC AGT AAA GAA AGA GTT ATT TTG AAG GTT ACG<br>Thr Ala Gln Gln Val Ser Ser Lys Glu Arg Val Ile Leu Lys Val Thr<br>1030 1035 1040                       |      |      | 624  |
| GTT CCG AGT GGG AAA GGT TCT ACT ACT CCA ACA AAA GCA GGT GTC ATT<br>Val Pro Ser Gly Lys Gly Ser Thr Thr Pro Thr Lys Ala Gly Val Ile<br>1045 1050 1055                       |      |      | 672  |
| TTA AAT AAT AGT GAA TAC AAA ATG CTC ATT GAT AAT GGG TAT ATG GTC<br><del>Leu Asn</del> Asn Ser Glu Tyr Lys Met Leu Ile <del>Asp</del> Asn Gly Tyr Met Val<br>1060 1065 1070 |      |      | 720  |
| CAT GTA GAT AAG GTA TCA AAA GTG GTG AAA AAA GGG GTG GAG TGC TTA<br>His Val Asp Lys Val Ser Lys Val Val Lys Lys Gly Val Glu Cys Leu<br>1075 1080 1085 1090                  |      |      | 768  |
| CAA ATT GAA GGG ACT TTA AAA AAG AGT CTT GAC TTT AAA AAT GAT ATA<br>Gln Ile Glu Gly Thr Leu Lys Lys Ser Leu Asp Phe Lys Asn Asp Ile<br>1095 1100 1105                       |      |      | 816  |
| AAT GCT GAA GCG CAT AGC TGG GGT ATG AAG AAT TAT GAA GAG TGG GCT<br>Asn Ala Glu Ala His Ser Trp Gly Met Lys Asn Tyr Glu Glu Trp Ala<br>1110 1115 1120                       |      |      | 864  |
| AAA GAT TTA ACC GAT TCG CAA AGG GAA GCT TTA GAT GGG TAT GCT AGG<br>Lys Asp Leu Thr Asp Ser Gln Arg Glu Ala Leu Asp Gly Tyr Ala Arg<br>1125 1130 1135                       |      |      | 912  |
| CAA GAT TAT AAA GAA ATC AAT AAT TAT TTA AGA AAT CAA GGC GGA AGT<br>Gln Asp Tyr Lys Glu Ile Asn Asn Tyr Leu Arg Asn Gln Gly Gly Ser<br>1140 1145 1150                       |      |      | 960  |
| GGA AAT GAA AAA CTA GAT GCT CAA ATA AAA AAT ATT TCT GAT GCT TTA<br>Gly Asn Glu Lys Leu Asp Ala Gln Ile Lys Asn Ile Ser Asp Ala Leu<br>1155 1160 1165 1170                  |      |      | 1008 |
| GGG AAG AAA CCA ATA CCG GAA AAT ATT ACT GTG TAT AGA TGG TGT GGC<br>Gly Lys Lys Pro Ile Pro Glu Asn Ile Thr Val Tyr Arg Trp Cys Gly<br>1175 1180 1185                       |      |      | 1056 |
| ATG CCG GAA TTT GGT TAT CAA ATT AGT GAT CCG TTA CCT TCT TTA AAA<br>Met Pro Glu Phe Gly Tyr Gln Ile Ser Asp Pro Leu Pro Ser Leu Lys<br>1190 1195 1200                       |      |      | 1104 |
| GAT TTT GAA GAA CAA TTT TTA AAT ACA ATC AAA GAA GAC AAA GGA TAT<br>Asp Phe Glu Glu Gln Phe Leu Asn Thr Ile Lys Glu Asp Lys Gly Tyr<br>1205 1210 1215                       |      |      | 1152 |
| ATG AGT ACA AGC TTA TCG AGT GAA CGT CTT GCA GCT TTT GGA TCT AGA<br>Met Ser Thr Ser Leu Ser Ser Glu Arg Leu Ala Ala Phe Gly Ser Arg<br>1220 1225 1230                       |      |      | 1200 |
| AAA ATT ATA TTA CGA TTA CAA GTT CCG AAA GGA AGT ACG GGT GCG TAT                                                                                                            |      |      | 1248 |

| Lys  | Ile  | Ile  | Leu  | Arg  | Leu  | Gln  | Val  | Pro  | Lys  | Gly | Ser | Thr  | Gly  | Ala  | Tyr  |      |
|------|------|------|------|------|------|------|------|------|------|-----|-----|------|------|------|------|------|
| 1235 |      |      |      |      |      |      |      |      |      |     |     |      |      |      |      | 1250 |
| TTA  | AGT  | GCC  | ATT  | GGT  | GGA  | TTT  | GCA  | AGT  | GAA  | AAA | GAG | ATC  | CTA  | CTT  | GAT  | 1296 |
| Leu  | Ser  | Ala  | Ile  | Gly  | Gly  | Phe  | Ala  | Ser  | Glu  | Lys | Glu | Ile  | Leu  | Leu  | Asp  |      |
|      |      |      |      | 1255 |      |      |      |      | 1260 |     |     |      |      |      | 1265 |      |
| AAA  | GAT  | AGT  | AAA  | TAT  | CAT  | ATT  | GAT  | AAA  | GTA  | ACA | GAG | GTA  | ATT  | ATT  | AAA  | 1344 |
| Lys  | Asp  | Ser  | Lys  | Tyr  | His  | Ile  | Asp  | Lys  | Val  | Thr | Glu | Val  | Ile  | Ile  | Lys  |      |
|      |      |      | 1270 |      |      |      |      | 1275 |      |     |     |      |      |      | 1280 |      |
| GGT  | GTT  | AAG  | CGA  | TAT  | GTA  | GTG  | GAT  | GCA  | ACA  | TTA | TTA | ACA  | AAT  | ATG  | AAA  | 1392 |
| Gly  | Val  | Lys  | Arg  | Tyr  | Val  | Val  | Asp  | Ala  | Thr  | Leu | Leu | Thr  | Asn  | Met  | Lys  |      |
|      |      | 1285 |      |      |      |      | 1290 |      |      |     |     |      | 1295 |      |      |      |
| AAT  | ATG  | AAG  | AAA  | AAG  | TTA  | GCA  | AGT  | GTT  | GTA  | ACG | TGT | ACG  | TTA  | TTA  | GCT  | 1440 |
| Asn  | Met  | Lys  | Lys  | Lys  | Leu  | Ala  | Ser  | Val  | Val  | Thr | Cys | Thr  | Leu  | Leu  | Ala  |      |
|      | 1300 |      |      |      |      | 1305 |      |      |      |     |     | 1310 |      |      |      |      |
| CCT  | ATG  | TTT  | TTG  | AAT  | GGA  | AAT  | GTG  | AAT  | GCT  | GTT | TAC | GCA  | GAC  | AGC  | AAA  | 1488 |
| Pro  | Met  | Phe  | Leu  | Asn  | Gly  | Asn  | Val  | Asn  | Ala  | Val | Tyr | Ala  | Asp  | Ser  | Lys  |      |
|      | 1315 |      |      |      | 1320 |      |      |      | 1325 |     |     |      |      |      | 1330 |      |
| ACA  | AAT  | CAA  | ATT  | TCT  | ACA  | ACA  | CAG  | AAA  | AAT  | CAA | CAG | AAA  | GAG  | ATG  | GAC  | 1536 |
| Thr  | Asn  | Gln  | Ile  | Ser  | Thr  | Thr  | Gln  | Lys  | Asn  | Gln | Gln | Lys  | Glu  | Met  | Asp  |      |
|      |      |      | 1335 |      |      |      |      | 1340 |      |     |     |      |      | 1345 |      |      |
| CGA  | AAA  | GGA  | TTA  | CTT  | GGG  | TAT  | TAT  | TTC  | AAA  | GGA | AAA | GAT  | TTT  | AGT  | AAT  | 1584 |
| Arg  | Lys  | Gly  | Leu  | Leu  | Gly  | Tyr  | Tyr  | Phe  | Lys  | Gly | Lys | Asp  | Phe  | Ser  | Asn  |      |
|      |      | 1350 |      |      |      |      |      | 1355 |      |     |     |      | 1360 |      |      |      |
| CTT  | ACT  | ATG  | TTT  | GCA  | CCG  | ACA  | CGT  | GAT  | AGT  | ACT | CTT | ATT  | TAT  | GAT  | CAA  | 1632 |
| Leu  | Thr  | Met  | Phe  | Ala  | Pro  | Thr  | Arg  | Asp  | Ser  | Thr | Leu | Ile  | Tyr  | Asp  | Gln  |      |
|      | 1365 |      |      |      |      |      | 1370 |      |      |     |     | 1375 |      |      |      |      |
| CAA  | ACA  | GCA  | AAT  | AAA  | CTA  | TTA  | GAT  | AAA  | AAA  | CAA | CAA | GAA  | TAT  | CAG  | TCT  | 1680 |
| Gln  | Thr  | Ala  | Asn  | Lys  | Leu  | Leu  | Asp  | Lys  | Lys  | Gln | Gln | Glu  | Tyr  | Gln  | Ser  |      |
|      | 1380 |      |      |      |      | 1385 |      |      |      |     |     | 1390 |      |      |      |      |
| ATT  | CGT  | TGG  | ATT  | GGT  | TTG  | ATT  | CAG  | AGT  | AAA  | GAA | ACG | GGA  | GAT  | TTC  | ACA  | 1728 |
| Ile  | Arg  | Trp  | Ile  | Gly  | Leu  | Ile  | Gln  | Ser  | Lys  | Glu | Thr | Gly  | Asp  | Phe  | Thr  |      |
|      | 1395 |      |      |      | 1400 |      |      |      | 1405 |     |     |      |      |      | 1410 |      |
| TTT  | AAC  | TTA  | TCT  | GAG  | GAT  | GAA  | CAG  | GCA  | ATT  | ATA | GAA | ATC  | AAT  | GGG  | AAA  | 1776 |
| Phe  | Asn  | Leu  | Ser  | Glu  | Asp  | Glu  | Gln  | Ala  | Ile  | Ile | Glu | Ile  | Asn  | Gly  | Lys  |      |
|      |      |      | 1415 |      |      |      |      | 1420 |      |     |     |      |      | 1425 |      |      |
| ATT  | ATT  | TCT  | AAT  | AAA  | GGG  | AAA  | GAA  | AAG  | CAA  | GTT | GTC | CAT  | TTA  | GAA  | AAA  | 1824 |
| Ile  | Ile  | Ser  | Asn  | Lys  | Gly  | Lys  | Glu  | Lys  | Gln  | Val | Val | His  | Leu  | Glu  | Lys  |      |
|      |      | 1430 |      |      |      |      | 1435 |      |      |     |     |      | 1440 |      |      |      |
| GGA  | AAA  | TTA  | GTT  | CCA  | ATC  | AAA  | ATA  | GAG  | TAT  | CAA | TCA | GAT  | ACA  | AAA  | TT   |      |



- 75 -

|                                                                                                                                                           |      |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| AAT ATT GAC AGT AAA ACA TTT AAA GAA CTT AAA TTA TTT AAA ATA GAT<br>Asn Ile Asp Ser Lys Thr Phe Lys Glu Leu Lys Leu Phe Lys Ile Asp<br>1460 1465 1470      | 1920 |
| AGT CAA AAC CAA CCC CAG CAA GTC CAG CAA GAT GAA CTG AGA AAT CCT<br>Ser Gln Asn Gln Pro Gln Gln Val Gln Gln Asp Glu Leu Arg Asn Pro<br>1475 1480 1485 1490 | 1968 |
| GAA TTT AAC AAG AAA GAA TCA CAG GAA TTC TTA GCG AAA CCA TCG AAA<br>Glu Phe Asn Lys Lys Glu Ser Gln Glu Phe Leu Ala Lys Pro Ser Lys<br>1495 1500 1505      | 2016 |
| ATA AAT CTT TTC ACT CAA AAA ATG AAA AGG GAA ATT GAT GAA GAC ACG<br>Ile Asn Leu Phe Thr Gln Lys Met Lys Arg Glu Ile Asp Glu Asp Thr<br>1510 1515 1520      | 2064 |
| GAT ACG GAT GGG GAC TCT ATT CCT GAC CTT TGG GAA GAA AAT GGG TAT<br>Asp Thr Asp Gly Asp Ser Ile Pro Asp Leu Trp Glu Glu Asn Gly Tyr<br>1525 1530 1535      | 2112 |
| ACG ATT CAA AAT AGA ATC GCT GTA AAG TGG GAC GAT TCT CTA GCA AGT<br>Thr Ile Gln Asn Arg Ile Ala Val Lys Trp Asp Asp Ser Leu Ala Ser<br>1540 1545 1550      | 2160 |
| AAA GGG TAT ACG AAA TTT GTT TCA AAT CCA CTA GAA AGT CAC ACA GTT<br>Lys Gly Tyr Thr Lys Phe Val Ser Asn Pro Leu Glu Ser His Thr Val<br>1555 1560 1565 1570 | 2208 |
| GGT GAT CCT TAT ACA GAT TAT GAA AAG GCA GCA AGA GAT CTA GAT TTG<br>Gly Asp Pro Tyr Thr Asp Tyr Glu Lys Ala Ala Arg Asp Leu Asp Leu<br>1575 1580 1585      | 2256 |
| TCA AAT GCA AAG GAA ACG TTT AAC CCA TTG GTA GCT GCT TTT CCA AGT<br>Ser Asn Ala Lys Glu Thr Phe Asn Pro Leu Val Ala Ala Phe Pro Ser<br>1590 1595 1600      | 2304 |
| GTG AAT GTT AGT ATG GAA AAG GTG ATA TTA TCA CCA AAT GAA AAT TTA<br>Val Asn Val Ser Met Glu Lys Val Ile Leu Ser Pro Asn Glu Asn Leu<br>1605 1610 1615      | 2352 |
| TCC AAT AGT GTA GAG TCT CAT TCA TCC ACG AAT TGG TCT TAT ACA AAT<br>Ser Asn Ser Val Glu Ser His Ser Ser Thr Asn Trp Ser Tyr Thr Asn<br>1620 1625 1630      | 2400 |
| ACA GAA GGT GCT TCT GTT GAA GCG GGG ATT GGA CCA AAA GGT ATT TCG<br>Thr Glu Gly Ala Ser Val Glu Ala Gly Ile Gly Pro Lys Gly Ile Ser<br>1635 1640 1645 1650 | 2448 |
| TTC GGA GTT AGC GTA AAC TAT CAA CAC TCT GAA ACA GTT GCA CAA GAA<br>Phe Gly Val Ser Val Asn Tyr Gln His Ser Glu Thr Val Ala Gln Glu<br>1655 1660 1665      | 2496 |
| TGG GGA ACA TCT ACA GGA AAT ACT TCG CAA TTC AAT ACG GCT TCA GCG<br>Trp Gly Thr Ser Thr Gly Asn Thr Ser Gln Phe Asn Thr Ala Ser Ala<br>1670 1675 1680      | 2544 |

- 76 -

|                                                                                                                                                           |      |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| GGA TAT TTA AAT GCA AAT GTT CGA TAT AAC AAT GTA GGA ACT GGT GCC<br>Gly Tyr Leu Asn Ala Asn Val Arg Tyr Asn Asn Val Gly Thr Gly Ala<br>1685 1690 1695      | 2592 |
| ATC TAC GAT GTA AAA CCT ACA ACA AGT TTT GTA TTA AAT AAC GAT ACT<br>Ile Tyr Asp Val Lys Pro Thr Thr Ser Phe Val Leu Asn Asn Asp Thr<br>1700 1705 1710      | 2640 |
| ATC GCA ACT ATT ACG GCG AAA TCT AAT TCT ACA GCC TTA AAT ATA TCT<br>Ile Ala Thr Ile Thr Ala Lys Ser Asn Ser Thr Ala Leu Asn Ile Ser<br>1715 1720 1725 1730 | 2688 |
| CCT GGA GAA AGT TAC CCG AAA AAA GGA CAA AAT GGA ATC GCA ATA ACA<br>Pro Gly Glu Ser Tyr Pro Lys Lys Gly Gln Asn Gly Ile Ala Ile Thr<br>1735 1740 1745      | 2736 |
| TCA ATG GAT GAT TTT AAT TCC CAT CCG ATT ACA TTA AAT AAA AAA CAA<br>Ser Met Asp Asp Phe Asn Ser His Pro Ile Thr Leu Asn Lys Lys Gln<br>1750 1755 1760      | 2784 |
| GTA GAT AAT CTG CTA AAT AAT AAA CCT ATG ATG TTG GAA ACA AAC CAA<br>Val Asp Asn Leu Leu Asn Asn Lys Pro Met Met Leu Glu Thr Asn Gln<br>1765 1770 1775      | 2832 |
| ACA GAT GGT GTT TAT AAG ATA AAA GAT ACA CAT GGA AAT ATA GTA ACT<br>Thr Asp Gly Val Tyr Lys Ile Lys Asp Thr His Gly Asn Ile Val Thr<br>1780 1785 1790      | 2880 |
| GGC GGA GAA TGG AAT GGT GTC ATA CAA CAA ATC AAG GCT AAA ACA GCG<br>Gly Gly Glu Trp Asn Gly Val Ile Gln Gln Ile Lys Ala Lys Thr Ala<br>1795 1800 1805 1810 | 2928 |
| TCT ATT ATT GTG GAT GAT GGG GAA CGT GTA GCA GAA AAA CGT GTA GCG<br>Ser Ile Ile Val Asp Asp Gly Glu Arg Val Ala Glu Lys Arg Val Ala<br>1815 1820 1825      | 2976 |
| GCA AAA GAT TAT GAA AAT CCA GAA GAT AAA ACA CCG TCT TTA ACT TTA<br>Ala Lys Asp Tyr Glu Asn Pro Glu Asp Lys Thr Pro Ser Leu Thr Leu<br>1830 1835 1840      | 3024 |
| AAA GAT GCC CTG AAG CTT TCA TAT CCA GAT GAA ATA AAA GAA ATA GAG<br>Lys Asp Ala Leu Lys Leu Ser Tyr Pro Asp Glu Ile Lys Glu Ile Glu<br>1845 1850 1855      | 3072 |
| GGA TTA TTA TAT TAT AAA AAC AAA CCG ATA TAC GAA TCG AGC GTT ATG<br>Gly Leu Leu Tyr Tyr Lys Asn Lys Pro Ile Tyr Glu Ser Ser Val Met<br>1860 1865 1870      | 3120 |
| ACT TAC TTA GAT GAA AAT ACA GCA AAA GAA GTG ACC AAA CAA TTA AAT<br>Thr Tyr Leu Asp Glu Asn Thr Ala Lys Glu Val Thr Lys Gln Leu Asn<br>1875 1880 1885 1890 | 3168 |
| GAT ACC ACT GGG AAA TTT AAA GAT GTA AGT CAT TTA TAT GAT GTA AAA<br>Asp Thr Thr Gly Lys Phe Lys Asp Val Ser His Leu Tyr Asp Val Lys                        | 3216 |

- 77 -

| 1895                                                                                                                                                      | 1900 | 1905 |      |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------|------|------|------|
| CTG ACT CCA AAA ATG AAT GTT ACA ATC AAA TTG TCT ATA CTT TAT GAT<br>Leu Thr Pro Lys Met Asn Val Thr Ile Lys Leu Ser Ile Leu Tyr Asp<br>1910 1915 1920      |      |      | 3264 |
| AAT GCT GAG TCT AAT GAT AAC TCA ATT GGT AAA TGG ACA AAC ACA AAT<br>Asn Ala Glu Ser Asn Asp Asn Ser Ile Gly Lys Trp Thr Asn Thr Asn<br>1925 1930 1935      |      |      | 3312 |
| ATT GTT TCA GGT GGA AAT AAC GGA AAA AAA CAA TAT TCT TCT AAT AAT<br>Ile Val Ser Gly Gly Asn Asn Gly Lys Lys Gln Tyr Ser Ser Asn Asn<br>1940 1945 1950      |      |      | 3360 |
| CCG GAT GCT AAT TTG ACA TTA AAT ACA GAT GCT CAA GAA AAA TTA AAT<br>Pro Asp Ala Asn Leu Thr Leu Asn Thr Asp Ala Gln Glu Lys Leu Asn<br>1955 1960 1965 1970 |      |      | 3408 |
| AAA AAT CGT GAC TAT TAT ATA AGT TTA TAT ATG AAG TCA GAA AAA AAC<br>Lys Asn Arg Asp Tyr Tyr Ile Ser Leu Tyr Met Lys Ser Glu Lys Asn<br>1975 1980 1985      |      |      | 3456 |
| ACA CAA TGT GAG ATT ACT ATA GAT GGG GAG ATT TAT CCG ATC ACT ACA<br>Thr Gln Cys Glu Ile Thr Ile Asp Gly Glu Ile Tyr Pro Ile Thr Thr<br>1990 1995 2000      |      |      | 3504 |
| AAA ACA GTG AAT GTG AAT AAA GAC AAT TAC AAA AGA TTA GAT ATT ATA<br>Lys Thr Val Asn Val Asn Lys Asp Asn Tyr Lys Arg Leu Asp Ile Ile<br>2005 2010 2015      |      |      | 3552 |
| GCT CAT AAT ATA AAA AGT AAT CCA ATT TCT TCA CTT CAT ATT AAA ACG<br>Ala His Asn Ile Lys Ser Asn Pro Ile Ser Ser Leu His Ile Lys Thr<br>2020 2025 2030      |      |      | 3600 |
| AAT GAT GAA ATA ACT TTA TTT TGG GAT GAT ATT TCT ATA ACA GAT GTA<br>Asn Asp Glu Ile Thr Leu Phe Trp Asp Asp Ile Ser Ile Thr Asp Val<br>2035 2040 2045 2050 |      |      | 3648 |
| GCA TCA ATA AAA CCG GAA AAT TTA ACA GAT TCA GAA ATT AAA CAG ATT<br>Ala Ser Ile Lys Pro Glu Asn Leu Thr Asp Ser Glu Ile Lys Gln Ile<br>2055 2060 2065      |      |      | 3696 |
| TAT AGT AGG TAT GGT ATT AAG TTA GAA GAT GGA ATC CTT ATT GAT AAA<br>Tyr Ser Arg Tyr Gly Ile Lys Leu Glu Asp Gly Ile Leu Ile Asp Lys<br>2070 2075 2080      |      |      | 3744 |
| AAA GGT GGG ATT CAT TAT GGT GAA TTT ATT AAT GAA GCT AGT TTT AAT<br>Lys Gly Gly Ile His Tyr Gly Glu Phe Ile Asn Glu Ala Ser Phe Asn<br>2085 2090 2095      |      |      | 3792 |
| ATT GAA CCA TTG CAA AAT TAT GTG ACC AAA TAT GAA GTT ACT TAT AGT<br>Ile Glu Pro Leu Gln Asn Tyr Val Thr Lys Tyr Glu Val Thr Tyr Ser<br>2100 2105 2110      |      |      | 3840 |
| AGT GAG TTA GGA CCA AAC GTG AGT GAC ACA CTT GAA AGT GAT AAA ATT                                                                                           |      |      | 3888 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1346 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:23:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Arg | Met | Glu | Gly | Lys | Leu | Phe | Met | Val | Ser | Lys | Lys | Leu | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Val | Thr | Lys | Thr | Val | Leu | Leu | Ser | Thr | Val | Phe | Ser | Ile | Ser | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Asn | Asn | Glu | Val | Ile | Lys | Ala | Glu | Gln | Leu | Asn | Ile | Asn | Ser | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Lys | Tyr | Thr | Asn | Leu | Gln | Asn | Leu | Lys | Ile | Thr | Asp | Lys | Val | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Phe | Lys | Glu | Asp | Lys | Glu | Lys | Ala | Lys | Glu | Trp | Gly | Lys | Glu | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Lys | Glu | Trp | Lys | Leu | Thr | Ala | Thr | Glu | Lys | Gly | Lys | Met | Asn | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Leu | Asp | Asn | Lys | Asn | Asp | Ile | Lys | Thr | Asn | Tyr | Lys | Glu | Ile | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Ser | Met | Ala | Gly | Ser | Phe | Glu | Asp | Glu | Ile | Lys | Asp | Leu | Lys | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

- 79 -

Ile Asp Lys Met Phe Asp Lys Thr Asn Leu Ser Asn Ser Ile Ile Thr  
 130 135 140  
 Tyr Lys Asn Val Glu Pro Thr Thr Ile Gly Phe Asn Lys Ser Leu Thr  
 145 150 155 160  
 Glu Gly Asn Thr Ile Asn Ser Asp Ala Met Ala Gln Phe Lys Glu Gln  
 165 170 175  
 Phe Leu Asp Arg Asp Ile Lys Phe Asp Ser Tyr Leu Asp Thr His Leu  
 180 185 190  
 Thr Ala Gln Gln Val Ser Ser Lys Glu Arg Val Ile Leu Lys Val Thr  
 195 200 205  
 Val Pro Ser Gly Lys Gly Ser Thr Thr Pro Thr Lys Ala Gly Val Ile  
 210 215 220  
 Leu Asn Asn Ser Glu Tyr Lys Met Leu Ile Asp Asn Gly Tyr Met Val  
 225 230 235 240  
 His Val Asp Lys Val Ser Lys Val Val Lys Lys Gly Val Glu Cys Leu  
 245 250 255  
 Gln Ile Glu Gly Thr Leu Lys Lys Ser Leu Asp Phe Lys Asn Asp Ile  
 260 265 270  
 Asn Ala Glu Ala His Ser Trp Gly Met Lys Asn Tyr Glu Glu Trp Ala  
 275 280 285  
 Lys Asp Leu Thr Asp Ser Gln Arg Glu Ala Leu Asp Gly Tyr Ala Arg  
 290 295 300  
 Gln Asp Tyr Lys Glu Ile Asn Asn Tyr Leu Arg Asn Gln Gly Gly Ser  
 305 310 315 320  
 Gly Asn Glu Lys Leu Asp Ala Gln Ile Lys Asn Ile Ser Asp Ala Leu  
 325 330 335  
 Gly Lys Lys Pro Ile Pro Glu Asn Ile Thr Val Tyr Arg Trp Cys Gly  
 340 345 350  
 Met Pro Glu Phe Gly Tyr Gln Ile Ser Asp Pro Leu Pro Ser Leu Lys  
 355 360 365  
 Asp Phe Glu Glu Gln Phe Leu Asn Thr Ile Lys Glu Asp Lys Gly Tyr  
 370 375 380  
 Met Ser Thr Ser Leu Ser Ser Glu Arg Leu Ala Ala Phe Gly Ser Arg  
 385 390 395 400  
 Lys Ile Ile Leu Arg Leu Gln Val Pro Lys Gly Ser Thr Gly Ala Tyr  
 405 410 415  
 Leu Ser Ala Ile Gly Gly Phe Ala Ser Glu Lys Glu Ile Leu Leu Asp

- 80 -

420 425 430  
 Lys Asp Ser Lys Tyr His Ile Asp Lys Val Thr Glu Val Ile Ile Lys  
 435 440 445  
 Gly Val Lys Arg Tyr Val Val Asp Ala Thr Leu Leu Thr Asn Met Lys  
 450 455 460  
 Asn Met Lys Lys Lys Leu Ala Ser Val Val Thr Cys Thr Leu Leu Ala  
 465 470 475 480  
 Pro Met Phe Leu Asn Gly Asn Val Asn Ala Val Tyr Ala Asp Ser Lys  
 485 490 495  
 Thr Asn Gln Ile Ser Thr Thr Gln Lys Asn Gln Gln Lys Glu Met Asp  
 500 505 510  
 Arg Lys Gly Leu Leu Gly Tyr Tyr Phe Lys Gly Lys Asp Phe Ser Asn  
 515 520 525  
 Leu Thr Met Phe Ala Pro Thr Arg Asp Ser Thr Leu Ile Tyr Asp Gln  
 530 535 540  
 Gln Thr Ala Asn Lys Leu Leu Asp Lys Lys Gln Gln Glu Tyr Gln Ser  
 545 550 555 560  
 Ile Arg Trp Ile Gly Leu Ile Gln Ser Lys Glu Thr Gly Asp Phe Thr  
 565 570 575  
 Phe Asn Leu Ser Glu Asp Glu Gln Ala Ile Ile Glu Ile Asn Gly Lys  
 580 585 590  
 Ile Ile Ser Asn Lys Gly Lys Glu Lys Gln Val Val His Leu Glu Lys  
 595 600 605  
 Gly Lys Leu Val Pro Ile Lys Ile Glu Tyr Gln Ser Asp Thr Lys Phe  
 610 615 620  
 Asn Ile Asp Ser Lys Thr Phe Lys Glu Leu Lys Leu Phe Lys Ile Asp  
 625 630 635 640  
 Ser Gln Asn Gln Pro Gln Gln Val Gln Gln Asp Glu Leu Arg Asn Pro  
 645 650 655  
 Glu Phe Asn Lys Lys Glu Ser Gln Glu Phe Leu Ala Lys Pro Ser Lys  
 660 665 670  
 Ile Asn Leu Phe Thr Gln Lys Met Lys Arg Glu Ile Asp Glu Asp Thr  
 675 680 685  
 Asp Thr Asp Gly Asp Ser Ile Pro Asp Leu Trp Glu Glu Asn Gly Tyr  
 690 695 700  
 Thr Ile Gln Asn Arg Ile Ala Val Lys Trp Asp Asp Ser Leu Ala Ser  
 705 710 715 720

- 81 -

Lys Gly Tyr Thr Lys Phe Val Ser Asn Pro Leu Glu Ser His Thr Val  
 725 730 735  
 Gly Asp Pro Tyr Thr Asp Tyr Glu Lys Ala Ala Arg Asp Leu Asp Leu  
 740 745 750  
 Ser Asn Ala Lys Glu Thr Phe Asn Pro Leu Val Ala Ala Phe Pro Ser  
 755 760 765  
 Val Asn Val Ser Met Glu Lys Val Ile Leu Ser Pro Asn Glu Asn Leu  
 770 775 780  
 Ser Asn Ser Val Glu Ser His Ser Ser Thr Asn Trp Ser Tyr Thr Asn  
 785 790 795 800  
 Thr Glu Gly Ala Ser Val Glu Ala Gly Ile Gly Pro Lys Gly Ile Ser  
 805 810 815  
 Phe Gly Val Ser Val Asn Tyr Gln His Ser Glu Thr Val Ala Gln Glu  
 820 825 830  
 Trp Gly Thr Ser Thr Gly Asn Thr Ser Gln Phe Asn Thr Ala Ser Ala  
 835 840 845  
 Gly Tyr Leu Asn Ala Asn Val Arg Tyr Asn Asn Val Gly Thr Gly Ala  
 850 855 860  
 Ile Tyr Asp Val Lys Pro Thr Thr Ser Phe Val Leu Asn Asn Asp Thr  
 865 870 875 880  
 Ile Ala Thr Ile Thr Ala Lys Ser Asn Ser Thr Ala Leu Asn Ile Ser  
 885 890 895  
 Pro Gly Glu Ser Tyr Pro Lys Lys Gly Gln Asn Gly Ile Ala Ile Thr  
 900 905 910  
 Ser Met Asp Asp Phe Asn Ser His Pro Ile Thr Leu Asn Lys Lys Gln  
 915 920 925  
 Val Asp Asn Leu Leu Asn Asn Lys Pro Met Met Leu Glu Thr Asn Gln  
 930 935 940  
 Thr Asp Gly Val Tyr Lys Ile Lys Asp Thr His Gly Asn Ile Val Thr  
 945 950 955 960  
 Gly Gly Glu Trp Asn Gly Val Ile Gln Gln Ile Lys Ala Lys Thr Ala  
 965 970 975  
 Ser Ile Ile Val Asp Asp Gly Glu Arg Val Ala Glu Lys Arg Val Ala  
 980 985 990  
 Ala Lys Asp Tyr Glu Asn Pro Glu Asp Lys Thr Pro Ser Leu Thr Leu  
 995 1000 1005

- 82 -

Lys Asp Ala Leu Lys Leu Ser Tyr Pro Asp Glu Ile Lys Glu Ile Glu  
 1010 1015 1020  
 Gly Leu Leu Tyr Tyr Lys Asn Lys Pro Ile Tyr Glu Ser Ser Val Met  
 1025 1030 1035 1040  
 Thr Tyr Leu Asp Glu Asn Thr Ala Lys Glu Val Thr Lys Gln Leu Asn  
 1045 1050 1055  
 Asp Thr Thr Gly Lys Phe Lys Asp Val Ser His Leu Tyr Asp Val Lys  
 1060 1065 1070  
 Leu Thr Pro Lys Met Asn Val Thr Ile Lys Leu Ser Ile Leu Tyr Asp  
 1075 1080 1085  
 Asn Ala Glu Ser Asn Asp Asn Ser Ile Gly Lys Trp Thr Asn Thr Asn  
 1090 1095 1100  
 Ile Val Ser Gly Gly Asn Asn Gly Lys Lys Gln Tyr Ser Ser Asn Asn  
 1105 1110 1115 1120  
 Pro Asp Ala Asn Leu Thr Leu Asn Thr Asp Ala Gln Glu Lys Leu Asn  
 1125 1130 1135  
 Lys Asn Arg Asp Tyr Tyr Ile Ser Leu Tyr Met Lys Ser Glu Lys Asn  
 1140 1145 1150  
 Thr Gln Cys Glu Ile Thr Ile Asp Gly Glu Ile Tyr Pro Ile Thr Thr  
 1155 1160 1165  
 Lys Thr Val Asn Val Asn Lys Asp Asn Tyr Lys Arg Leu Asp Ile Ile  
 1170 1175 1180  
 Ala His Asn Ile Lys Ser Asn Pro Ile Ser Ser Leu His Ile Lys Thr  
 1185 1190 1195 1200  
 Asn Asp Glu Ile Thr Leu Phe Trp Asp Asp Ile Ser Ile Thr Asp Val  
 1205 1210 1215  
 Ala Ser Ile Lys Pro Glu Asn Leu Thr Asp Ser Glu Ile Lys Gln Ile  
 1220 1225 1230  
 Tyr Ser Arg Tyr Gly Ile Lys Leu Glu Asp Gly Ile Leu Ile Asp Lys  
 1235 1240 1245  
 Lys Gly Gly Ile His Tyr Gly Glu Phe Ile Asn Glu Ala Ser Phe Asn  
 1250 1255 1260  
 Ile Glu Pro Leu Gln Asn Tyr Val Thr Lys Tyr Glu Val Thr Tyr Ser  
 1265 1270 1275 1280  
 Ser Glu Leu Gly Pro Asn Val Ser Asp Thr Leu Glu Ser Asp Lys Ile  
 1285 1290 1295  
 Tyr Lys Asp Gly Thr Ile Lys Phe Asp Phe Thr Lys Tyr Ser Lys Asn



- 83 -

1300                      1305                      1310  
 Glu Gln Gly Leu Phe Tyr Asp Ser Gly Leu Asn Trp Asp Phe Lys Ile  
                          1315                      1320                      1325  
 Asn Ala Ile Thr Tyr Asp Gly Lys Glu Met Asn Val Phe His Arg Tyr  
                          1330                      1335                      1340  
 Asn Lys  
 1345

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..1386
- (D) OTHER INFORMATION: /note= "Maize optimized DNA sequence for VIP2A(a) protein from AB78"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ATGAAGCGCA TGGAGGGCAA GCTGTTTCATG GTGAGCAAGA AGCTCCAGGT GGTGACCAAG | 60  |
| ACCGTGCTGC TGAGCACCGT GTTCAGCATC AGCCTGCTGA ACAACGAGGT GATCAAGGCC  | 120 |
| GAGCAGCTGA ACATCAACAG CCAGAGCAAG TACACCAACC TCCAGAACCT GAAGATCACC  | 180 |
| GACAAGGTGG AGGACTTCAA GGAGGACAAG GAGAAGGCCA AGGAGTGGGG CAAGGAGAAG  | 240 |
| GAGAAGGAGT GGAAGCTTAC CGCCACCGAG AAGGGCAAGA TGAACAACCTT CCTGGACAAC | 300 |
| AAGAACGACA TCAAGACCAA CTACAAGGAG ATCACCTTCA GCATGGCCGG CAGCTTCGAG  | 360 |
| GACGAGATCA AGGACCTGAA GGAGATCGAC AAGATGTTTG ACAAGACCAA CCTGAGCAAC  | 420 |
| AGCATCATCA CCTACAAGAA CGTGGAGCCC ACCACCATCG GCTTCAACAA GAGCCTGACC  | 480 |
| GAGGGCAACA CCATCAACAG CGACGCCATG GCCCAGTTCA AGGAGCAGTT CCTGGACCGC  | 540 |
| GACATCAAGT TCGACAGCTA CCTGGACACC CACCTGACCG CCCAGCAGGT GAGCAGCAAG  | 600 |
| GAGCGCGTGA TCCTGAAGGT GACCGTCCCC AGCGGCAAGG GCAGCACCAC CCCCACCAAG  | 660 |
| GCCGGCGTGA TCCTGAACAA CAGCGAGTAC AAGATGCTGA TCGACAACGG CTACATGGTG  | 720 |

- 84 -

```

CACGTGGACA AGGTGAGCAA GGTGGTGAAG AAGGGCGTGG AGTGCCTCCA GATCGAGGGC 780
ACCCTGAAGA AGAGTCTAGA CTTCAAGAAC GACATCAACG CCGAGGCCCA CAGCTGGGGC 840
ATGAAGAACT ACGAGGAGTG GGCCAAGGAC CTGACCGACA GCCAGCGCGA GGCCCTGGAC 900
GGCTACGCCC GCCAGGACTA CAAGGAGATC AACAACTACC TGCGCAACCA GGGCGGCAGC 960
GGCAACGAGA AGCTGGACGC CCAGATCAAG AACATCAGCG ACGCCCTGGG CAAGAAGCCC 1020
ATCCCCGAGA ACATCACCGT GTACCGCTGG TGGGCATGC CCGAGTTGG CTACCAGATC 1080
AGCGACCCCC TGCCAGCCT GAAGGACTTC GAGGAGCAGT TCCTGAACAC CATCAAGGAG 1140
GACAAGGGCT ACATGAGCAC CAGCCTGAGC AGCGAGCGCC TGGCCGCTT CCGCAGCOGC 1200
AAGATCATCC TGGCCTGCA GGTGCCCAAG GGCAGCACCG GCGCCTACCT GAGCGCCATC 1260
GGCGGCTTCG CCAGCGAGAA GGAGATCCTG CTGGACAAGG ACAGCAAGTA CCACATCGAC 1320
AAGGTGACCG AGGTGATCAT CAAGGGCGTG AAGCGCTACG TGGTGGACGC CACCTGCTG 1380
ACCAACTAGA TCTGAGCTC 1399

```

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "Secretion signal peptide to secrete VIP2 out of a cell"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly Val
1 5 10 15

```

```

His Cys Leu

```

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2655 base pairs
- (B) TYPE: nucleic acid

- 85 -

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..2655  
(D) OTHER INFORMATION: /note= "maize optimized DNA  
sequence encoding VIPIA(a)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ATGAAGAACA TGAAGAAGAA GCTGGCCAGC GTGGTGACCT GCACCCCTGCT GGCCCCCATG | 60   |
| TTCTTGAACG GCAACGTGAA CGCCGTGTAC GCGACAGCA AGACCAACCA GATCAGCACC   | 120  |
| ACCCAGAAGA ACCAGCAGAA GGAGATGGAC CGCAAGGGCC TGCTGGGCTA CTACTTCAAG  | 180  |
| GGCAAGGACT TCAGCAACCT GACCATGTTT GCCCCACGC GTGACAGCAC CCTGATCTAC   | 240  |
| GACCAGCAGA CCGCCAACAA GCTGCTGGAC AAGAAGCAGC AGGAGTACCA GAGCATCCGC  | 300  |
| TGGATCGGCC TGATCCAGAG CAAGGAGACC GGCGACTTCA CCTTCAACCT GAGCGAGGAC  | 360  |
| GAGCAGGCCA TCATOGAGAT CAACGGCAAG ATCATCAGCA ACAAGGGCAA GGAGAAGCAG  | 420  |
| GTGGTGCAAC TGGAGAAGGG CAAGCTGGTG CCCATCAAGA TCGAGTACCA GAGCGACACC  | 480  |
| AAGTTCAACA TCGACAGCAA GACCTTCAAG GAGCTGAAGC TTTTCAAGAT CGACAGCCAG  | 540  |
| AACCAGCCCC AGCAGGTGCA GCAGGACGAG CTGCGCAACC CCGAGTTCAA CAAGAAGGAG  | 600  |
| AGCCAGGAGT TCCTGGCCAA GCCCAGCAAG ATCAACCTGT TCACCCAGCA GATGAAGCGC  | 660  |
| GAGATCGACG AGGACACCGA CACCGACGGC GACAGCATCC CCGACCTGTG GGAGGAGAAC  | 720  |
| GGCTACACCA TCCAGAACCG CATCGCCGTG AAGTGGGACG ACAGCCTGGC TAGCAAGGGC  | 780  |
| TACACCAAGT TCGTGAGCAA CCCCTGGAG AGCCACACCG TGGGCGACCC CTACACCGAC   | 840  |
| TACGAGAAGG CCGCCCGGGA CCTGGACCTG AGCAACGCCA AGGAGACCTT CAACCCCTG   | 900  |
| GTGGCCGCCT TCCCCAGCGT GAACGTGAGC ATGGAGAAGG TGATCCTGAG CCCCACGAG   | 960  |
| AACCTGAGCA ACAGCGTGA GAGCCACTCG AGCACCAACT GGAGCTACAC CAACACCGAG   | 1020 |
| GGCGCCAGCG TGGAGGCCGG CATCGGTCCC AAGGGCATCA GCTTCGGCGT GAGCGTGAAC  | 1080 |
| TACCAGCACA GCGAGACCGT GGGCCAGGAG TGGGGCACCA GCACCGCAA CACCAGCCAG   | 1140 |

- 86 -

|                                                                   |      |
|-------------------------------------------------------------------|------|
| TTCAACACCG CCAGCGCCCG CTACCTGAAC GCCAACGTGC GCTACAACAA CGTGGGCACC | 1200 |
| GGCGCCATCT ACGACGTGAA GCCCACCACC AGCTTCGTGC TGAACAACGA CACCATCGCC | 1260 |
| ACCATCACCG CCAAGTCGAA TTCCACCGCC CTGAACATCA GCCCCGGCGA GAGCTACCCC | 1320 |
| AAGAAGGGCC AGAACGGCAT CGCCATCACC AGCATGGACG ACTTCAACAG CCACCCCATC | 1380 |
| ACCTGAACA AGAAGCAGGT GGACAACCTG CTGAACAACA AGCCCATGAT GCTGGAGACC  | 1440 |
| AACCAGACCG ACGGCGTCTA CAAGATCAAG GACACCCACG GCAACATCGT GACGGGCGGC | 1500 |
| GAGTGAACG GCGTGATCCA GCAGATCAAG GCCAAGACCG CCAGCATCAT CGTCGACGAC  | 1560 |
| GGGAGCGCG TGGCCGAGAA GCGCGTGGCC GCCAAGGACT ACGAGAACCC CGAGGACAAG  | 1620 |
| ACCCCCAGCC TGACCCTGAA GGACGCCCTG AAGCTGAGCT ACCCCGACGA GATCAAGGAG | 1680 |
| ATCGAGGGCT TGCTGTACTA CAAGAACAAG CCCATCTACG AGAGCAGCGT GATGACCTAT | 1740 |
| CTAGACGAGA ACACCGCCAA GGAGGTGACC AAGCAGCTGA ACGACACCAC CGGCAAGTTC | 1800 |
| AAGGACGTGA GCCACCTGTA CGAOGTGAAG CTGACCCCCA AGATGAACGT GACCATCAAG | 1860 |
| CTGAGCATCC TGTACGACAA CGCGAGAGC AACGACAACA GCATCGGCAA GTGGACCAAC  | 1920 |
| ACCAACATCG TGAGCGGGG CAACAACGGC AAGAAGCAGT ACAGCAGCAA CAACCCCGAC  | 1980 |
| GCCAACCTGA CCTGAACAC CGACGCCCAG GAGAAGCTGA ACAAGAACCG CGACTACTAC  | 2040 |
| ATCAGCCTGT ACATGAAGAG CGAGAAGAAC ACCCAGTGCG AGATCACCAT CGACGGCGAG | 2100 |
| ATATACCCCA TCACCACCAA GACCGTGAAC GTGAACAAGG ACAACTACAA GCGCCTGGAC | 2160 |
| ATCATCGCCC ACAACATCAA GAGCAACCCC ATCAGCAGCC TGCACATCAA GACCAACGAC | 2220 |
| GAGATCACCC TGTTCCTGGA CGACATATCG ATTACGACG TCGCCAGCAT CAAGCCCGAG  | 2280 |
| AACCTGACCG ACAGCGAGAT CAAGCAGATA TACAGTCGCT ACGGCATCAA GCTGGAGGAC | 2340 |
| GGCATCCTGA TCGACAAGAA AGGCGGCATC CACTACGGCG AGTTCATCAA CGAGGCCAGC | 2400 |
| TTCAACATCG AGCCCCTGCA GAACTACGTG ACCAAGTACG AGGTGACCTA CAGCAGCGAG | 2460 |
| CTGGGCCCCA ACGTGAGCGA CACCCTGGAG AGCGACAAGA TTTACAAGGA CGGCACCATC | 2520 |
| AAGTTCGACT TCACCAAGTA CAGCAAGAAC GAGCAGGGCC TGTTCACGA CAGCGGCTG   | 2580 |
| AACTGGGACT TCAAGATCAA CGCCATCACC TACGACGGCA AGGAGATGAA CGTGTTCAC  | 2640 |
| CGCTACAACA AGTAG                                                  | 2655 |

(2) INFORMATION FOR SEQ ID NO:27:

- 87 -

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

## (iii) HYPOTHETICAL: NO

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..1389
- (D) OTHER INFORMATION: /note= "maize optimized DNA sequence encoding VIP2A(a) "

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ATGAAGCGCA TGGAGGGCAA GCTGTTTCATG GTGAGCAAGA AGCTCCAGGT GGTGACCAAG | 60   |
| ACCGTGCTGC TGAGCACCGT GTTCAGCATC AGCCTGCTGA ACAACGAGGT GATCAAGGCC  | 120  |
| GAGCAGCTGA ACATCAACAG CCAGAGCAAG TACACCAACC TCCAGAACCT GAAGATCACC  | 180  |
| GACAAGGTGG AGGACTTCAA GGAGGACAAG GAGAAGGCCA AGGAGTGGGG CAAGGAGAAG  | 240  |
| GAGAAGGAGT GGAAGCTTAC CGCCACCGAG AAGGGCAAGA TGAACAACCTT CCTGGACAAC | 300  |
| AAGAACGACA TCAAGACCAA CTACAAGGAG ATCACCTTCA GCATAGCCGG CAGCTTCGAG  | 360  |
| GACGAGATCA AGGACCTGAA GGAGATCGAC AAGATGTTTC ACAAGACCAA CCTGAGCAAC  | 420  |
| AGCATCATCA CCTACAAGAA CGTGGAGCCC ACCACCATCG GCTTCAACAA GAGCCTGACC  | 480  |
| GAGGGCAACA CCATCAACAG CGACGCCATG GCCAGTTTCA AGGAGCAGTT CCTGGACCGC  | 540  |
| GACATCAAGT TCGACAGCTA CCTGGACACC CACCTGACCG CCCAGCAGGT GAGCAGCAAG  | 600  |
| GAGCGCGTGA TCCTGAAGGT GACCGTCCCC AGCGGCAAGG GCAGCACCAC CCCCACCAAG  | 660  |
| GCCGGCGTGA TCCTGAACAA CAGCGAGTAC AAGATGCTGA TCGACAACGG CTACATGGTG  | 720  |
| CACGTGGACA AGGTGAGCAA GGTGGTGAAG AAGGGCGTGG AGTGCCTCCA GATOGAGGGC  | 780  |
| ACCTGAAGA AGAGTCTAGA CTTCAAGAAC GACATCAACG CCGAGGCCCA CAGCTGGGGC   | 840  |
| ATGAAGAACT ACGAGGAGTG GGCCAAGGAC CTGACCGACA GCCAGCGGA GGCCTGGAC    | 900  |
| GGCTACGCCC GCCAGGACTA CAAGGAGATC AACAACTACC TGCGCAACCA GGGCGGCAGC  | 960  |
| GGCAACGAGA AGCTGGACGC CCAGATCAAG AACATCAGCG ACGCCCTGGG CAAGAAGCCC  | 1020 |

- 88 -

ATCCCCGAGA ACATCACCGT GTACCGCTGG TGCGGCATGC CCGAGTTCGG CTACCAGATC 1080  
 AGCGACCCCC TGCCCAGCCT GAAGGACTTC GAGGAGCAGT TCCTGAACAC CATCAAGGAG 1140  
 GACAAGGGCT ACATGAGCAC CAGCCTGAGC AGCGAGCGCC TGGCCGCTT CGGCAGCCGC 1200  
 AAGATCATCC TGCGCTGCA GGTGCCAAG GGCAGCACTG GTGCCTACCT GAGCGCCATC 1260  
 GGCGGCTTCG CCAGCGAGAA GGAGATCCTG CTGGATAAGG ACAGCAAGTA CCACATCGAC 1320  
 AAGGTGACCG AGGTGATCAT CAAGGGCGTG AAGCGCTACG TGGTGGACGC CACCCTGCTG 1380  
 ACCAACTAG 1389

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 9..2375
- (D) OTHER INFORMATION: /note= "Native DNA sequence encoding VIP3A(a) protein from AB88 as contained in pCIB7104"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGATGAAC ATG AAC AAG AAT AAT ACT AAA TTA AGC ACA AGA GCC TTA CCA 50  
 Met Asn Lys Asn Asn Thr Lys Leu Ser Thr Arg Ala Leu Pro  
 1 5 10

AGT TTT ATT GAT TAT TTT AAT GGC ATT TAT GGA TTT GCC ACT GGT ATC 98  
 Ser Phe Ile Asp Tyr Phe Asn Gly Ile Tyr Gly Phe Ala Thr Gly Ile  
 15 20 25 30

AAA GAC ATT ATG AAC ATG ATT TTT AAA ACG GAT ACA GGT GGT GAT CTA 146  
 Lys Asp Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Asp Leu  
 35 40 45

ACC CTA GAC GAA ATT TTA AAG AAT CAG CAG TTA CTA AAT GAT ATT TCT 194  
 Thr Leu Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Asp Ile Ser  
 50 55 60

GGT AAA TTG GAT GGG GTG AAT GGA AGC TTA AAT GAT CTT ATC GCA CAG 242  
 Gly Lys Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln  
 65 70 75

- 89 -

|                                                                                                                                                       |     |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| GGA AAC TTA AAT ACA GAA TTA TCT AAG GAA ATA TTA AAA ATT GCA AAT<br>Gly Asn Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys Ile Ala Asn<br>80 85 90        | 290 |
| GAA CAA AAT CAA GTT TTA AAT GAT GTT AAT AAC AAA CTC GAT GCG ATA<br>Glu Gln Asn Gln Val Leu Asn Asp Val Asn Asn Lys Leu Asp Ala Ile<br>95 100 105 110  | 338 |
| AAT ACG ATG CTT CGG GTA TAT CTA CCT AAA ATT ACC TCT ATG TTG AGT<br>Asn Thr Met Leu Arg Val Tyr Leu Pro Lys Ile Thr Ser Met Leu Ser<br>115 120 125     | 386 |
| GAT GTA ATG AAA CAA AAT TAT GCG CTA AGT CTG CAA ATA GAA TAC TTA<br>Asp Val Met Lys Gln Asn Tyr Ala Leu Ser Leu Gln Ile Glu Tyr Leu<br>130 135 140     | 434 |
| AGT AAA CAA TTG CAA GAG ATT TCT GAT AAG TTG GAT ATT ATT AAT GTA<br>Ser Lys Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Ile Ile Asn Val<br>145 150 155     | 482 |
| AAT GTA CTT ATT AAC TCT ACA CTT ACT GAA ATT ACA CCT GCG TAT CAA<br>Asn Val Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln<br>160 165 170     | 530 |
| AGG ATT AAA TAT GTG AAC GAA AAA TTT GAG GAA TTA ACT TTT GCT ACA<br>Arg Ile Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr Phe Ala Thr<br>175 180 185 190 | 578 |
| GAA ACT AGT TCA AAA GTA AAA AAG GAT GGC TCT CCT GCA GAT ATT CTT<br>Glu Thr Ser Ser Lys Val Lys Lys Asp Gly Ser Pro Ala Asp Ile Leu<br>195 200 205     | 626 |
| GAT GAG TTA ACT GAG TTA ACT GAA CTA GCG AAA AGT GTA ACA AAA AAT<br>Asp Glu Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn<br>210 215 220     | 674 |
| GAT GTG GAT GGT TTT GAA TTT TAC CTT AAT ACA TTC CAC GAT GTA ATG<br>Asp Val Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met<br>225 230 235     | 722 |
| GTA GGA AAT AAT TTA TTC GGG CGT TCA GCT TTA AAA ACT GCA TCG GAA<br>Val Gly Asn Asn Leu Phe Gly Arg Ser Ala Leu Lys Thr Ala Ser Glu<br>240 245 250     | 770 |
| TTA ATT ACT AAA GAA AAT GTG AAA ACA AGT GGC AGT GAG GTC GGA AAT<br>Leu Ile Thr Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn<br>255 260 265 270 | 818 |
| GTT TAT AAC TTC TTA ATT GTA TTA ACA GCT CTG CAA GCC CAA GCT TTT<br>Val Tyr Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Gln Ala Phe<br>275 280 285     | 866 |
| CTT ACT TTA ACA ACA TGC CGA AAA TTA TTA GGC TTA GCA GAT ATT GAT<br>Leu Thr Leu Thr Thr Cys Arg Lys Leu Leu Gly Leu Ala Asp Ile Asp<br>914             | 914 |

- 90 -

| 290                                                                                                                                                   | 295 | 300 |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----|------|
| TAT ACT TCT ATT ATG AAT GAA CAT TTA AAT AAG GAA AAA GAG GAA TTT<br>Tyr Thr Ser Ile Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe<br>305 310 315     |     |     | 962  |
| AGA GTA AAC ATC CTC CCT ACA CTT TCT AAT ACT TTT TCT AAT CCT AAT<br>Arg Val Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn<br>320 325 330     |     |     | 1010 |
| TAT GCA AAA GTT AAA GGA AGT GAT GAA GAT GCA AAG ATG ATT GTG GAA<br>Tyr Ala Lys Val Lys Gly Ser Asp Glu Asp Ala Lys Met Ile Val Glu<br>335 340 345 350 |     |     | 1058 |
| GCT AAA CCA GGA CAT GCA TTG ATT GGG TTT GAA ATT AGT AAT GAT TCA<br>Ala Lys Pro Gly His Ala Leu Ile Gly Phe Glu Ile Ser Asn Asp Ser<br>355 360 365     |     |     | 1106 |
| ATT ACA GTA TTA AAA GTA TAT GAG GCT AAG CTA AAA CAA AAT TAT CAA<br>Ile Thr Val Leu Lys Val Tyr Glu Ala Lys Leu Lys Gln Asn Tyr Gln<br>370 375 380     |     |     | 1154 |
| GTC GAT AAG GAT TCC TTA TCG GAA GTT ATT TAT GGT GAT ATG GAT AAA<br>Val Asp Lys Asp Ser Leu Ser Glu Val Ile Tyr Gly Asp Met Asp Lys<br>385 390 395     |     |     | 1202 |
| TTA TTG TGC CCA GAT CAA TCT GAA CAA ATC TAT TAT ACA AAT AAC ATA<br>Leu Leu Cys Pro Asp Gln Ser Glu Gln Ile Tyr Tyr Thr Asn Asn Ile<br>400 405 410     |     |     | 1250 |
| GTA TTT CCA AAT GAA TAT GTA ATT ACT AAA ATT GAT TTC ACT AAA AAA<br>Val Phe Pro Asn Glu Tyr Val Ile Thr Lys Ile Asp Phe Thr Lys Lys<br>415 420 425 430 |     |     | 1298 |
| ATG AAA ACT TTA AGA TAT GAG GTA ACA GCG AAT TTT TAT GAT TCT TCT<br>Met Lys Thr Leu Arg Tyr Glu Val Thr Ala Asn Phe Tyr Asp Ser Ser<br>435 440 445     |     |     | 1346 |
| ACA GGA GAA ATT GAC TTA AAT AAG AAA AAA GTA GAA TCA AGT GAA GCG<br>Thr Gly Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser Ser Glu Ala<br>450 455 460     |     |     | 1394 |
| GAG TAT AGA ACG TTA AGT GCT AAT GAT GAT GGG GTG TAT ATG CCG TTA<br>Glu Tyr Arg Thr Leu Ser Ala Asn Asp Asp Gly Val Tyr Met Pro Leu<br>465 470 475     |     |     | 1442 |
| GGT GTC ATC AGT GAA ACA TTT TTG ACT CCG ATT AAT GGG TTT GGC CTC<br>Gly Val Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Leu<br>480 485 490     |     |     | 1490 |
| CAA GCT GAT GAA AAT TCA AGA TTA ATT ACT TTA ACA TGT AAA TCA TAT<br>Gln Ala Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys Lys Ser Tyr<br>495 500 505 510 |     |     | 1538 |
| TTA AGA GAA CTA CTG CTA GCA ACA GAC TTA AGC AAT AAA GAA ACT AAA                                                                                       |     |     | 1586 |



- 91 -

|                                                                 |      |
|-----------------------------------------------------------------|------|
| Leu Arg Glu Leu Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys |      |
| 515 520 525                                                     |      |
| TTG ATC GTC CCG CCA AGT GGT TTT ATT AGC AAT ATT GTA GAG AAC GGG | 1634 |
| Leu Ile Val Pro Ser Gly Phe Ile Ser Asn Ile Val Glu Asn Gly     |      |
| 530 535 540                                                     |      |
| TCC ATA GAA GAG GAC AAT TTA GAG CCG TGG AAA GCA AAT AAT AAG AAT | 1682 |
| Ser Ile Glu Glu Asp Asn Leu Glu Pro Trp Lys Ala Asn Asn Lys Asn |      |
| 545 550 555                                                     |      |
| GCG TAT GTA GAT CAT ACA GGC GGA GTG AAT GGA ACT AAA GCT TTA TAT | 1730 |
| Ala Tyr Val Asp His Thr Gly Gly Val Asn Gly Thr Lys Ala Leu Tyr |      |
| 560 565 570                                                     |      |
| GTT CAT AAG GAC GGA GGA ATT TCA CAA TTT ATT GGA GAT AAG TTA AAA | 1778 |
| Val His Lys Asp Gly Gly Ile Ser Gln Phe Ile Gly Asp Lys Leu Lys |      |
| 575 580 585 590                                                 |      |
| CCG AAA ACT GAG TAT GTA ATC CAA TAT ACT GTT AAA GGA AAA CCT TCT | 1826 |
| Pro Lys Thr Glu Tyr Val Ile Gln Tyr Thr Val Lys Gly Lys Pro Ser |      |
| 595 600 605                                                     |      |
| ATT CAT TTA AAA GAT GAA AAT ACT GGA TAT ATT CAT TAT GAA GAT ACA | 1874 |
| Ile His Leu Lys Asp Glu Asn Thr Gly Tyr Ile His Tyr Glu Asp Thr |      |
| 610 615 620                                                     |      |
| AAT AAT AAT TTA GAA GAT TAT CAA ACT ATT AAT AAA CGT TTT ACT ACA | 1922 |
| Asn Asn Asn Leu Glu Asp Tyr Gln Thr Ile Asn Lys Arg Phe Thr Thr |      |
| 625 630 635                                                     |      |
| GGA ACT GAT TTA AAG GGA GTG TAT TTA ATT TTA AAA AGT CAA AAT GGA | 1970 |
| Gly Thr Asp Leu Lys Gly Val Tyr Leu Ile Leu Lys Ser Gln Asn Gly |      |
| 640 645 650                                                     |      |
| GAT GAA GCT TGG GGA GAT AAC TTT ATT ATT TTG GAA ATT AGT CCT TCT | 2018 |
| Asp Glu Ala Trp Gly Asp Asn Phe Ile Ile Leu Glu Ile Ser Pro Ser |      |
| 655 660 665 670                                                 |      |
| GAA AAG TTA TTA AGT CCA GAA TTA ATT AAT ACA AAT AAT TGG ACG AGT | 2066 |
| Glu Lys Leu Leu Ser Pro Glu Leu Ile Asn Thr Asn Asn Trp Thr Ser |      |
| 675 680 685                                                     |      |
| ACG GGA TCA ACT AAT ATT AGC GGT AAT ACA CTC ACT CTT TAT CAG GGA | 2114 |
| Thr Gly Ser Thr Asn Ile Ser Gly Asn Thr Leu Thr Leu Tyr Gln Gly |      |
| 690 695 700                                                     |      |
| GGA CGA GGG ATT CTA AAA CAA AAC CTT CAA TTA GAT AGT TTT TCA ACT | 2162 |
| Gly Arg Gly Ile Leu Lys Gln Asn Leu Gln Leu Asp Ser Phe Ser Thr |      |
| 705 710 715                                                     |      |
| TAT AGA GTG TAT TTT TCT GTG TCC GGA GAT GCT AAT GTA AGG ATT AGA | 2210 |
| Tyr Arg Val Tyr Phe Ser Val Ser Gly Asp Ala Asn Val Arg Ile Arg |      |
| 720 725 730                                                     |      |

|                                                                 |      |
|-----------------------------------------------------------------|------|
| AAT TCT AGG GAA GTG TTA TTT GAA AAA AGA TAT ATG AGC GGT GCT AAA | 2258 |
| Asn Ser Arg Glu Val Leu Phe Glu Lys Arg Tyr Met Ser Gly Ala Lys |      |
| 735 740 745 750                                                 |      |
| GAT GTT TCT GAA ATG TTC ACT ACA AAA TTT GAG AAA GAT AAC TTT TAT | 2306 |
| Asp Val Ser Glu Met Phe Thr Thr Lys Phe Glu Lys Asp Asn Phe Tyr |      |
| 755 760 765                                                     |      |
| ATA GAG CTT TCT CAA GGG AAT AAT TTA TAT GGT GGT CCT ATT GTA CAT | 2354 |
| Ile Glu Leu Ser Gln Gly Asn Asn Leu Tyr Gly Gly Pro Ile Val His |      |
| 770 775 780                                                     |      |
| TTT TAC GAT GTC TCT ATT AAG TAA                                 | 2378 |
| Phe Tyr Asp Val Ser Ile Lys                                     |      |
| 785                                                             |      |

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 789 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Lys | Asn | Asn | Thr | Lys | Leu | Ser | Thr | Arg | Ala | Leu | Pro | Ser | Phe |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |
| Ile | Asp | Tyr | Phe | Asn | Gly | Ile | Tyr | Gly | Phe | Ala | Thr | Gly | Ile | Lys | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Met | Asn | Met | Ile | Phe | Lys | Thr | Asp | Thr | Gly | Gly | Asp | Leu | Thr | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Glu | Ile | Leu | Lys | Asn | Gln | Gln | Leu | Leu | Asn | Asp | Ile | Ser | Gly | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Asp | Gly | Val | Asn | Gly | Ser | Leu | Asn | Asp | Leu | Ile | Ala | Gln | Gly | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Asn | Thr | Glu | Leu | Ser | Lys | Glu | Ile | Leu | Lys | Ile | Ala | Asn | Glu | Gln |
|     |     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |
| Asn | Gln | Val | Leu | Asn | Asp | Val | Asn | Asn | Lys | Leu | Asp | Ala | Ile | Asn | Thr |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Met | Leu | Arg | Val | Tyr | Leu | Pro | Lys | Ile | Thr | Ser | Met | Leu | Ser | Asp | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Met | Lys | Gln | Asn | Tyr | Ala | Leu | Ser | Leu | Gln | Ile | Glu | Tyr | Leu | Ser | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

- 93 -

Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Ile Ile Asn Val Asn Val  
 145 150 155 160  
 Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Ile  
 165 170 175  
 Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr Phe Ala Thr Glu Thr  
 180 185 190  
 Ser Ser Lys Val Lys Lys Asp Gly Ser Pro Ala Asp Ile Leu Asp Glu  
 195 200 205  
 Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp Val  
 210 215 220  
 Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met Val Gly  
 225 230 235 240  
 Asn Asn Leu Phe Gly Arg Ser Ala Leu Lys Thr Ala Ser Glu Leu Ile  
 245 250 255  
 Thr Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn Val Tyr  
 260 265 270  
 Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Gln Ala Phe Leu Thr  
 275 280 285  
 Leu Thr Thr Cys Arg Lys Leu Leu Gly Leu Ala Asp Ile Asp Tyr Thr  
 290 295 300  
 Ser Ile Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe Arg Val  
 305 310 315 320  
 Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Ala  
 325 330 335  
 Lys Val Lys Gly Ser Asp Glu Asp Ala Lys Met Ile Val Glu Ala Lys  
 340 345 350  
 Pro Gly His Ala Leu Ile Gly Phe Glu Ile Ser Asn Asp Ser Ile Thr  
 355 360 365  
 Val Leu Lys Val Tyr Glu Ala Lys Leu Lys Gln Asn Tyr Gln Val Asp  
 370 375 380  
 Lys Asp Ser Leu Ser Glu Val Ile Tyr Gly Asp Met Asp Lys Leu Leu  
 385 390 395 400  
 Cys Pro Asp Gln Ser Glu Gln Ile Tyr Tyr Thr Asn Asn Ile Val Phe  
 405 410 415  
 Pro Asn Glu Tyr Val Ile Thr Lys Ile Asp Phe Thr Lys Lys Met Lys  
 420 425 430  
 Thr Leu Arg Tyr Glu Val Thr Ala Asn Phe Tyr Asp Ser Ser Thr Gly

- 94 -

|                                                                                    |     |     |
|------------------------------------------------------------------------------------|-----|-----|
| 435                                                                                | 440 | 445 |
| Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser Ser Glu Ala Glu Tyr<br>450 455 460     |     |     |
| Arg Thr Leu Ser Ala Asn Asp Asp Gly Val Tyr Met Pro Leu Gly Val<br>465 470 475 480 |     |     |
| Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Leu Gln Ala<br>485 490 495     |     |     |
| Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys Lys Ser Tyr Leu Arg<br>500 505 510     |     |     |
| Glu Leu Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys Leu Ile<br>515 520 525     |     |     |
| Val Pro Pro Ser Gly Phe Ile Ser Asn Ile Val Glu Asn Gly Ser Ile<br>530 535 540     |     |     |
| Glu Glu Asp Asn Leu Glu Pro Trp Lys Ala Asn Asn Lys Asn Ala Tyr<br>545 550 555 560 |     |     |
| Val Asp His Thr Gly Gly Val Asn Gly Thr Lys Ala Leu Tyr Val His<br>565 570 575     |     |     |
| Lys Asp Gly Gly Ile Ser Gln Phe Ile Gly Asp Lys Leu Lys Pro Lys<br>580 585 590     |     |     |
| Thr Glu Tyr Val Ile Gln Tyr Thr Val Lys Gly Lys Pro Ser Ile His<br>595 600 605     |     |     |
| Leu Lys Asp Glu Asn Thr Gly Tyr Ile His Tyr Glu Asp Thr Asn Asn<br>610 615 620     |     |     |
| Asn Leu Glu Asp Tyr Gln Thr Ile Asn Lys Arg Phe Thr Thr Gly Thr<br>625 630 635 640 |     |     |
| Asp Leu Lys Gly Val Tyr Leu Ile Leu Lys Ser Gln Asn Gly Asp Glu<br>645 650 655     |     |     |
| Ala Trp Gly Asp Asn Phe Ile Ile Leu Glu Ile Ser Pro Ser Glu Lys<br>660 665 670     |     |     |
| Leu Leu Ser Pro Glu Leu Ile Asn Thr Asn Asn Trp Thr Ser Thr Gly<br>675 680 685     |     |     |
| Ser Thr Asn Ile Ser Gly Asn Thr Leu Thr Leu Tyr Gln Gly Gly Arg<br>690 695 700     |     |     |
| Gly Ile Leu Lys Gln Asn Leu Gln Leu Asp Ser Phe Ser Thr Tyr Arg<br>705 710 715 720 |     |     |
| Val Tyr Phe Ser Val Ser Gly Asp Ala Asn Val Arg Ile Arg Asn Ser<br>725 730 735     |     |     |

- 95 -

Arg Glu Val Leu Phe Glu Lys Arg Tyr Met Ser Gly Ala Lys Asp Val  
                   740                  745                  750

Ser Glu Met Phe Thr Thr Lys Phe Glu Lys Asp Asn Phe Tyr Ile Glu  
                   755                  760                  765

Leu Ser Gln Gly Asn Asn Leu Tyr Gly Gly Pro Ile Val His Phe Tyr  
                   770                  775                  780

Asp Val Ser Ile Lys  
                   785

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 11..2389
- (D) OTHER INFORMATION: /note= "maize optimized DNA sequence encoding VIP3A(a)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| GGATCCACCA ATGAACATGA ACAAGAACAA CACCAAGCTG AGCACCCGCG CCCTGCCGAG  | 60  |
| CTTCATCGAC TACTTCAACG GCATCTACGG CTTGCCACC GGCATCAAGG ACATCATGAA   | 120 |
| CATGATCTTC AAGACCGACA CCGGGGGGGA CCTGACCTG GACGAGATCC TGAAGAACCA   | 180 |
| GCAGCTGCTG AACGACATCA GCGGCAAGCT GGACGGGCTG AACGGCAGCC TGAACGACCT  | 240 |
| GATCGCCCAG GGCAACCTGA ACACCGAGCT GAGCAAGGAG ATCCTTAAGA TCGCCAACGA  | 300 |
| GCAGAACCCAG GTGCTGAACG ACGTGAACAA CAAGCTGGAC GCCATCAACA CCATGCTGCG | 360 |
| CGTGTACCTG CCGAAGATCA CCAGCATGCT GAGCGACGTG ATGAAGCAGA ACTACGCCCT  | 420 |
| GAGCCTGCAG ATCGAGTACC TGAGCAAGCA GCTGCAGGAG ATCAGCGACA AGCTGGACAT  | 480 |
| CATCAACGTG AACGTCTTGA TCAACAGCAC CCTGACCGAG ATCACCCCGG CTTACCAGCG  | 540 |
| CATCAAGTAC GTGAACGAGA AGTTGAAGA GCTGACCTTC GCCACCGAGA CCAGCAGCAA   | 600 |

GGTGAAGAAG GACGGCAGCC CGGCCGACAT CCTGGACGAG CTGACCGAGC TGACCGAGCT 660  
GGCCAAGAGC GTGACCAAGA ACGACGTGGA CGGCTTCGAG TTCTACCTGA ACACCTTCCA 720  
CGACGTGATG GTGGGCAACA ACCTGTTGGG CCGCAGCGCC CTGAAGACCG CCAGCGAGCT 780  
GATCACC AAG GAGAACGTGA AGACCAGCGG CAGCGAGGTG GGCAACGTGT ACAACTTCCT 840  
GATCGTGCTG ACCGCCCTGC AGGCCAGGC CTTCCTGACC CTGACCACCT GTCGCAAGCT 900  
GCTGGGCTG GCCGACATCG ACTACACCAG CATCATGAAC GAGCACTTGA ACAAGGAGAA 960  
GGAGGAGTTC CGGTGAACA TCCTGCCGAC CCTGAGCAAC ACCTTCAGCA ACCCGAACTA 1020  
CGCCAAGGTG AAGGGCAGCG ACGAGGACGC CAAGATGATC GTGGAGGCTA AGCCGGGCCA 1080  
CGCGTTGATC GGCTTCGAGA TCAGCAACGA CAGCATCACC GTGCTGAAGG TGTACGAGGC 1140  
CAAGCTGAAG CAGAACTACC AGGTGGACAA GGACAGCTTG AGCGAGGTGA TCTACGGCGA 1200  
CATGGACAAG CTGCTGTGTC CGGACCAGAG CGAGCAAATC TACTACACCA ACAACATOGT 1260  
GTTCOCGAAC GAGTACGTGA TCACCAAGAT CGACTTCACC AAGAAGATGA AGACCTGCG 1320  
CTACGAGGTG ACCGCCAACT TCTACGACAG CAGCACCGGC GAGATCGACC TGAACAAGAA 1380  
GAAGGTGGAG AGCAGCGAGG CCGAGTACCG CACCCTGAGC GCGAACGACG ACCGGCTCTA 1440  
CATGCCACTG GGCGTGATCA GCGAGACCTT CCTGACCCCG ATCAACGGCT TTGGCCTGCA 1500  
GGCCGACGAG AACAGCCGCC TGATCACCTT GACCTGTAAG AGCTACCTGC GCGAGCTGCT 1560  
GCTAGCCACC GACCTGAGCA ACAAGGAGAC CAAGCTGATC GTGCCACCGA GCGGCTTCAT 1620  
CAGCAACATC GTGGAGAACG GCAGCATCGA GGAGGACAAC CTGGAGCCGT GGAAGGCCAA 1680  
CAACAAGAAC GCCTACGTGG ACCACACCGG CGCGTGAAAC GGCACCAAGG CCCTGTACGT 1740  
GCACAAGGAC GCGGCATCA GCCAGTTCAT CGCGACAAG CTGAAGCCGA AGACCGAGTA 1800  
CGTGATCCAG TACACCGTGA AGGGCAAGCC ATCGATTAC CTGAAGGACG AGAACACCGG 1860  
CTACATCCAC TACGAGGACA CCAACAACAA CCTGGAGGAC TACCAGACCA TCAACAAGCG 1920  
CTTCAACCACC GGCACCGACC TGAAGGGCGT GTACCTGATC CTGAAGAGCC AGAACGGCGA 1980  
CGAGGCCTGG GCGGCAACT TCATCATCCT GGAGATCAGC CCGAGCGAGA AGCTGCTGAG 2040  
CCCGGAGCTG ATCAACACCA ACAACTGGAC CAGCACCGGC AGCACCAACA TCAGCGGCAA 2100  
CACCCTGACC CTGTACCAGG GCGGCCGCGG CATCCTGAAG CAGAACCTGC AGCTGGACAG 2160  
CTTCAGCACC TACCGCGTGT ACTTCAGCGT GAGCGGCGAC GCCAACGTGC GCATCCGCAA 2220

- 97 -

CAGCCGCGAG GTGCTGTTCG AGAAGAGGTA CATGAGCGGC GCCAAGGACG TGAGCGAGAT 2280  
 GTTCACCACC AAGTTCGAGA AGGACAACTT CTACATCGAG CTGAGCCAGG GCAACAACCT 2340  
 GTACGGCGGC CCGATCGTGC ACTTCTACGA CGTGAGCATC AAGTTAACGT AGAGCTCAGA 2400  
 TCT 2403

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: -2612 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 118..2484
- (D) OTHER INFORMATION: /note= "Native DNA sequence encoding VIP3A(b) from AB424"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATTGAAATTG ATAAAAAGTT ATGAGTGTTC AATAATCAGT AATTACCAAT AAAGAATTAA 60  
 GAATACAAGT TTACAAGAAA TAAGTGTTC AAAAAATAGC TGAAAAGGAA GATGAAC 117  
 ATG AAC AAG AAT AAT ACT AAA TTA AGC ACA AGA GCC TTA CCA AGT TTT 165  
 Met Asn Lys Asn Asn Thr Lys Leu Ser Thr Arg Ala Leu Pro Ser Phe  
 790 795 800 805  
 ATT GAT TAT TTC AAT GGC ATT TAT GGA TTT GCC ACT GGT ATC AAA GAC 213  
 Ile Asp Tyr Phe Asn Gly Ile Tyr Gly Phe Ala Thr Gly Ile Lys Asp  
 810 815 820  
 ATT ATG AAC ATG ATT TTT AAA ACG GAT ACA GGT GGT GAT CTA ACC CTA 261  
 Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Asp Leu Thr Leu  
 825 830 835  
 GAC GAA ATT TTA AAG AAT CAG CAG CTA CTA AAT GAT ATT TCT GGT AAA 309  
 Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Asp Ile Ser Gly Lys  
 840 845 850  
 TTG GAT GGG GTG AAT GGA AGC TTA AAT GAT CTT ATC GCA CAG GGA AAC 357  
 Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln Gly Asn  
 855 860 865  
 TTA AAT ACA GAA TTA TCT AAG GAA ATA TTA AAA ATT GCA AAT GAA CAA 405

- 98 -

|                                                                                                                                                           |      |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys Ile Ala Asn Glu Gln<br>870 875 880 885                                                                        |      |
| AAT CAA GTT TTA AAT GAT GTT AAT AAC AAA CTC GAT GCG ATA AAT ACG<br>Asn Gln Val Leu Asn Asp Val Asn Asn Lys Leu Asp Ala Ile Asn Thr<br>890 895 900         | 453  |
| ATG CTT CGG GTA TAT CTA CCT AAA ATT ACC TCT ATG TTG AGT GAT GTA<br>Met Leu Arg Val Tyr Leu Pro Lys Ile Thr Ser Met Leu Ser Asp Val<br>905 910 915         | 501  |
| ATG AAA CAA AAT TAT GCG CTA AGT CTG CAA ATA GAA TAC TTA AGT AAA<br>Met Lys Gln Asn Tyr Ala Leu Ser Leu Gln Ile Glu Tyr Leu Ser Lys<br>920 925 930         | 549  |
| CAA TTG CAA GAG ATT TCT GAT AAG TTG GAT ATT ATT AAT GTA AAT GTA<br>Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Ile Ile Asn Val Asn Val<br>935 940 945         | 597  |
| CTT ATT AAC TCT ACA CTT ACT GAA ATT ACA CCT GCG TAT CAA AGG ATT<br>Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Ile<br>950 955 960 965     | 645  |
| AAA TAT GTG AAC GAA AAA TTT GAG GAA TTA ACT TTT GCT ACA GAA ACT<br>Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr Phe Ala Thr Glu Thr<br>970 975 980         | 693  |
| AGT TCA AAA GTA AAA AAG GAT GGC TCT CCT GCA GAT ATT CGT GAT GAG<br>Ser Ser Lys Val Lys Lys Asp Gly Ser Pro Ala Asp Ile Arg Asp Glu<br>985 990 995         | 741  |
| TTA ACT GAG TTA ACT GAA CTA GCG AAA AGT GTA ACA AAA AAT GAT GTG<br>Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp Val<br>1000 1005 1010      | 789  |
| GAT GGT TTT GAA TTT TAC CTT AAT ACA TTC CAC GAT GTA ATG GTA GGA<br>Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met Val Gly<br>1015 1020 1025      | 837  |
| AAT AAT TTA TTC GGG CGT TCA GCT TTA AAA ACT GCA TCG GAA TTA ATT<br>Asn Asn Leu Phe Gly Arg Ser Ala Leu Lys Thr Ala Ser Glu Leu Ile<br>1030 1035 1040 1045 | 885  |
| ACT AAA GAA AAT GTG AAA ACA AGT GGC AGT GAG GTC GGA AAT GTT TAT<br>Thr Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn Val Tyr<br>1050 1055 1060      | 933  |
| AAC TTC CTA ATT GTA TTA ACA GCT CTG CAA GCA AAA GCT TTT CTT ACT<br>Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Lys Ala Phe Leu Thr<br>1065 1070 1075      | 981  |
| TTA ACA CCA TGC CGA AAA TTA TTA GGC TTA GCA GAT ATT GAT TAT ACT<br>Leu Thr Pro Cys Arg Lys Leu Leu Gly Leu Ala Asp Ile Asp Tyr Thr<br>1080 1085 1090      | 1029 |



- 99 -

|                                                                                                                                                           |      |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| TCT ATT ATG AAT GAA CAT TTA AAT AAG GAA AAA GAG GAA TTT AGA GTA<br>Ser Ile Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe Arg Val<br>1095 1100 1105      | 1077 |
| AAC ATC CTC CCT ACA CTT TCT AAT ACT TTT TCT AAT CCT AAT TAT GCA<br>Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Ala<br>1110 1115 1120 1125 | 1125 |
| AAA GTT AAA GGA AGT GAT GAA GAT GCA AAG ATG ATT GTG GAA GCT AAA<br>Lys Val Lys Gly Ser Asp Glu Asp Ala Lys Met Ile Val Glu Ala Lys<br>1130 1135 1140      | 1173 |
| CCA GGA CAT GCA TTG ATT GGG TTT GAA ATT AGT AAT GAT TCA ATT ACA<br>Pro Gly His Ala Leu Ile Gly Phe Glu Ile Ser Asn Asp Ser Ile Thr<br>1145 1150 1155      | 1221 |
| GTA TTA AAA GTA TAT GAG GCT AAG CTA AAA CAA AAT TAT CAA GTC GAT<br>Val Leu Lys Val Tyr Glu Ala Lys Leu Lys Gln Asn Tyr Gln Val Asp<br>1160 1165 1170      | 1269 |
| AAG GAT TCC TTA TCG GAA GTT ATT TAT GGC GAT ATG GAT AAA TTA TTG<br>Lys Asp Ser Leu Ser Glu Val Ile Tyr Gly Asp Met Asp Lys Leu Leu<br>1175 1180 1185      | 1317 |
| TGC CCA GAT CAA TCT GGA CAA ATC TAT TAT ACA AAT AAC ATA GTA TTT<br>Cys Pro Asp Gln Ser Gly Gln Ile Tyr Tyr Thr Asn Asn Ile Val Phe<br>1190 1195 1200 1205 | 1365 |
| CCA AAT GAA TAT GTA ATT ACT AAA ATT GAT TTC ACT AAA AAA ATG AAA<br>Pro Asn Glu Tyr Val Ile Thr Lys Ile Asp Phe Thr Lys Lys Met Lys<br>1210 1215 1220      | 1413 |
| ACT TTA AGA TAT GAG GTA ACA GCG AAT TTT TAT GAT TCT TCT ACA GGA<br>Thr Leu Arg Tyr Glu Val Thr Ala Asn Phe Tyr Asp Ser Ser Thr Gly<br>1225 1230 1235      | 1461 |
| GAA ATT GAC TTA AAT AAG AAA AAA GTA GAA TCA AGT GAA GCG GAG TAT<br>Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser Ser Glu Ala Glu Tyr<br>1240 1245 1250      | 1509 |
| AGA ACG TTA AGT GCT AAT GAT GAT GGG GTG TAT ATG CCG TTA GGT GTC<br>Arg Thr Leu Ser Ala Asn Asp Asp Gly Val Tyr Met Pro Leu Gly Val<br>1255 1260 1265      | 1557 |
| ATC AGT GAA ACA TTT TTG ACT CCG ATT AAT GGG TTT GGC CTC CAA GCT<br>Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Leu Gln Ala<br>1270 1275 1280 1285 | 1605 |
| GAT GAA AAT TCA AGA TTA ATT ACT TTA ACA TGT AAA TCA TAT TTA AGA<br>Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys Lys Ser Tyr Leu Arg<br>1290 1295 1300      | 1653 |
| GAA CTA CTG CTA GCA ACA GAC TTA AGC AAT AAA GAA ACT AAA TTG ATC<br>Glu Leu Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys Leu Ile<br>1305 1310 1315      | 1701 |

- 100 -

|                                                                                                                                                           |      |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| GTC CCG CCA AGT GGT TTT ATT AGC AAT ATT GTA GAG AAC GGG TCC ATA<br>Val Pro Pro Ser Gly Phe Ile Ser Asn Ile Val Glu Asn Gly Ser Ile<br>1320 1325 1330      | 1749 |
| GAA GAG GAC AAT TTA GAG CCG TGG AAA GCA AAT AAT AAG AAT GCG TAT<br>Glu Glu Asp Asn Leu Glu Pro Trp Lys Ala Asn Asn Lys Asn Ala Tyr<br>1335 1340 1345      | 1797 |
| GTA GAT CAT ACA GGC GGA GTG AAT GGA ACT AAA GCT TTA TAT GTT CAT<br>Val Asp His Thr Gly Gly Val Asn Gly Thr Lys Ala Leu Tyr Val His<br>1350 1355 1360 1365 | 1845 |
| AAG GAC GGA GGA ATT TCA CAA TTT ATT GGA GAT AAG TTA AAA CCG AAA<br>Lys Asp Gly Gly Ile Ser Gln Phe Ile Gly Asp Lys Leu Lys Pro Lys<br>1370 1375 1380      | 1893 |
| ACT GAG TAT GTA ATC CAA TAT ACT GTT AAA GGA AAA CCT TCT ATT CAT<br>Thr Glu Tyr Val Ile Gln Tyr Thr Val Lys Gly Lys Pro Ser Ile His<br>1385 1390 1395      | 1941 |
| TTA AAA GAT GAA AAT ACT GGA TAT ATT CAT TAT GAA GAT ACA AAT AAT<br>Leu Lys Asp Glu Asn Thr Gly Tyr Ile His Tyr Glu Asp Thr Asn Asn<br>1400 1405 1410      | 1989 |
| AAT TTA GAA GAT TAT CAA ACT ATT AAT AAA CGT TTT ACT ACA GGA ACT<br>Asn Leu Glu Asp Tyr Gln Thr Ile Asn Lys Arg Phe Thr Thr Gly Thr<br>1415 1420 1425      | 2037 |
| GAT TTA AAG GGA GTG TAT TTA ATT TTA AAA AGT CAA AAT GGA GAT GAA<br>Asp Leu Lys Gly Val Tyr Leu Ile Leu Lys Ser Gln Asn Gly Asp Glu<br>1430 1435 1440 1445 | 2085 |
| GCT TGG GGA GAT AAC TTT ATT ATT TTG GAA ATT AGT CCT TCT GAA AAG<br>Ala Trp Gly Asp Asn Phe Ile Ile Leu Glu Ile Ser Pro Ser Glu Lys<br>1450 1455 1460      | 2133 |
| TTA TTA AGT CCA GAA TTA ATT AAT ACA AAT AAT TGG ACG AGT ACG GGA<br>Leu Leu Ser Pro Glu Leu Ile Asn Thr Asn Asn Trp Thr Ser Thr Gly<br>1465 1470 1475      | 2181 |
| TCA ACT AAT ATT AGC GGT AAT ACA CTC ACT CTT TAT CAG GGA GGA CGA<br>Ser Thr Asn Ile Ser Gly Asn Thr Leu Thr Leu Tyr Gln Gly Gly Arg<br>1480 1485 1490      | 2229 |
| GGG ATT CTA AAA CAA AAC CTT CAA TTA GAT AGT TTT TCA ACT TAT AGA<br>Gly Ile Leu Lys Gln Asn Leu Gln Leu Asp Ser Phe Ser Thr Tyr Arg<br>1495 1500 1505      | 2277 |
| GTG TAT TTC TCT GTG TCC GGA GAT GCT AAT GTA AGG ATT AGA AAT TCT<br>Val Tyr Phe Ser Val Ser Gly Asp Ala Asn Val Arg Ile Arg Asn Ser<br>1510 1515 1520 1525 | 2325 |
| AGG GAA GTG TTA TTT GAA AAA AGA TAT ATG AGC GGT GCT AAA GAT GTT<br>Arg Glu Val Leu Phe Glu Lys Arg Tyr Met Ser Gly Ala Lys Asp Val                        | 2373 |

- 101 -

|                                                                    |      |      |      |
|--------------------------------------------------------------------|------|------|------|
| 1530                                                               | 1535 | 1540 |      |
| TCT GAA ATG TTC ACT ACA AAA TTT GAG AAA GAT AAC TTC TAT ATA GAG    |      |      | 2421 |
| Ser Glu Met Phe Thr Thr Lys Phe Glu Lys Asp Asn Phe Tyr Ile Glu    |      |      |      |
| 1545                                                               | 1550 | 1555 |      |
| CTT TCT CAA GGG AAT AAT TTA TAT GGT GGT CCT ATT GTA CAT TTT TAC    |      |      | 2469 |
| Leu Ser Gln Gly Asn Asn Leu Tyr Gly Gly Pro Ile Val His Phe Tyr    |      |      |      |
| 1560                                                               | 1565 | 1570 |      |
| GAT GTC TCT ATT AAG TAAGATCGGG ATCTAATATT AACAGTTTTT AGAAGCTAAT    |      |      | 2524 |
| Asp Val Ser Ile Lys                                                |      |      |      |
| 1575                                                               |      |      |      |
| TCTTGATATAA TGTCCTTGAT TATGGAAAAA CACAATTTTG TTTGCTAAGA TGTATATATA |      |      | 2584 |
| GCTCACTCAT TAAAAGGCAA TCAAGCTT                                     |      |      | 2612 |

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Lys | Asn | Asn | Thr | Lys | Leu | Ser | Thr | Arg | Ala | Leu | Pro | Ser | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Asp | Tyr | Phe | Asn | Gly | Ile | Tyr | Gly | Phe | Ala | Thr | Gly | Ile | Lys | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Met | Asn | Met | Ile | Phe | Lys | Thr | Asp | Thr | Gly | Gly | Asp | Leu | Thr | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Glu | Ile | Leu | Lys | Asn | Gln | Gln | Leu | Leu | Asn | Asp | Ile | Ser | Gly | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Asp | Gly | Val | Asn | Gly | Ser | Leu | Asn | Asp | Leu | Ile | Ala | Gln | Gly | Asn |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Asn | Thr | Glu | Leu | Ser | Lys | Glu | Ile | Leu | Lys | Ile | Ala | Asn | Glu | Gln |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asn | Gln | Val | Leu | Asn | Asp | Val | Asn | Asn | Lys | Leu | Asp | Ala | Ile | Asn | Thr |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Met | Leu | Arg | Val | Tyr | Leu | Pro | Lys | Ile | Thr | Ser | Met | Leu | Ser | Asp | Val |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Met | Lys | Gln | Asn | Tyr | Ala | Leu | Ser | Leu | Gln | Ile | Glu | Tyr | Leu | Ser | Lys |

- 102 -

|                                                                 |     |         |
|-----------------------------------------------------------------|-----|---------|
| 130                                                             | 135 | 140     |
| Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Ile Ile Asn Val Asn Val |     |         |
| 145                                                             | 150 | 155 160 |
| Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Ile |     |         |
|                                                                 | 165 | 170 175 |
| Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr Phe Ala Thr Glu Thr |     |         |
|                                                                 | 180 | 185 190 |
| Ser Ser Lys Val Lys Lys Asp Gly Ser Pro Ala Asp Ile Arg Asp Glu |     |         |
|                                                                 | 195 | 200 205 |
| Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp Val |     |         |
|                                                                 | 210 | 215 220 |
| Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met Val Gly |     |         |
| 225                                                             | 230 | 235 240 |
| Asn Asn Leu Phe Gly Arg Ser Ala Leu Lys Thr Ala Ser Glu Leu Ile |     |         |
|                                                                 | 245 | 250 255 |
| Thr Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn Val Tyr |     |         |
|                                                                 | 260 | 265 270 |
| Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Lys Ala Phe Leu Thr |     |         |
|                                                                 | 275 | 280 285 |
| Leu Thr Pro Cys Arg Lys Leu Leu Gly Leu Ala Asp Ile Asp Tyr Thr |     |         |
|                                                                 | 290 | 295 300 |
| Ser Ile Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe Arg Val |     |         |
| 305                                                             | 310 | 315 320 |
| Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Ala |     |         |
|                                                                 | 325 | 330 335 |
| Lys Val Lys Gly Ser Asp Glu Asp Ala Lys Met Ile Val Glu Ala Lys |     |         |
|                                                                 | 340 | 345 350 |
| Pro Gly His Ala Leu Ile Gly Phe Glu Ile Ser Asn Asp Ser Ile Thr |     |         |
|                                                                 | 355 | 360 365 |
| Val Leu Lys Val Tyr Glu Ala Lys Leu Lys Gln Asn Tyr Gln Val Asp |     |         |
|                                                                 | 370 | 375 380 |
| Lys Asp Ser Leu Ser Glu Val Ile Tyr Gly Asp Met Asp Lys Leu Leu |     |         |
| 385                                                             | 390 | 395 400 |
| Cys Pro Asp Gln Ser Gly Gln Ile Tyr Tyr Thr Asn Asn Ile Val Phe |     |         |
|                                                                 | 405 | 410 415 |
| Pro Asn Glu Tyr Val Ile Thr Lys Ile Asp Phe Thr Lys Lys Met Lys |     |         |
|                                                                 | 420 | 425 430 |

- 103 -

Thr Leu Arg Tyr Glu Val Thr Ala Asn Phe Tyr Asp Ser Ser Thr Gly  
 435 440 445  
 Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser Ser Glu Ala Glu Tyr  
 450 455 460  
 Arg Thr Leu Ser Ala Asn Asp Asp Gly Val Tyr Met Pro Leu Gly Val  
 465 470 475 480  
 Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Leu Gln Ala  
 485 490 495  
 Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys Lys Ser Tyr Leu Arg  
 500 505 510  
 Glu Leu Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys Leu Ile  
 515 520 525  
 Val Pro Pro Ser Gly Phe Ile Ser Asn Ile Val Glu Asn Gly Ser Ile  
 530 535 540  
 Glu Glu Asp Asn Leu Glu Pro Trp Lys Ala Asn Asn Lys Asn Ala Tyr  
 545 550 555 560  
 Val Asp His Thr Gly Gly Val Asn Gly Thr Lys Ala Leu Tyr Val His  
 565 570 575  
 Lys Asp Gly Gly Ile Ser Gln Phe Ile Gly Asp Lys Leu Lys Pro Lys  
 580 585 590  
 Thr Glu Tyr Val Ile Gln Tyr Thr Val Lys Gly Lys Pro Ser Ile His  
 595 600 605  
 Leu Lys Asp Glu Asn Thr Gly Tyr Ile His Tyr Glu Asp Thr Asn Asn  
 610 615 620  
 Asn Leu Glu Asp Tyr Gln Thr Ile Asn Lys Arg Phe Thr Thr Gly Thr  
 625 630 635 640  
 Asp Leu Lys Gly Val Tyr Leu Ile Leu Lys Ser Gln Asn Gly Asp Glu  
 645 650 655  
 Ala Trp Gly Asp Asn Phe Ile Ile Leu Glu Ile Ser Pro Ser Glu Lys  
 660 665 670  
 Leu Leu Ser Pro Glu Leu Ile Asn Thr Asn Asn Trp Thr Ser Thr Gly  
 675 680 685  
 Ser Thr Asn Ile Ser Gly Asn Thr Leu Thr Leu Tyr Gln Gly Gly Arg  
 690 695 700  
 Gly Ile Leu Lys Gln Asn Leu Gln Leu Asp Ser Phe Ser Thr Tyr Arg  
 705 710 715 720

- 104 -

Val Tyr Phe Ser Val Ser Gly Asp Ala Asn Val Arg Ile Arg Asn Ser  
                               725                              730                              735

Arg Glu Val Leu Phe Glu Lys Arg Tyr Met Ser Gly Ala Lys Asp Val  
                               740                              745                              750

Ser Glu Met Phe Thr Thr Lys Phe Glu Lys Asp Asn Phe Tyr Ile Glu  
                               755                              760                              765

Leu Ser Gln Gly Asn Asn Leu Tyr Gly Gly Pro Ile Val His Phe Tyr  
                               770                              775                              780

Asp Val Ser Ile Lys  
 785

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "forward primer used to make pCIB5526"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGATCCACCA TGAAGACCAA CCAGATCAGC

30

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "reverse primer used to make pCIB5526"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

- 105 -

AAGCTTCAGC TCCTT

15

## (2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA"

## (iii) HYPOTHETICAL: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 9..2564
- (D) OTHER INFORMATION: /note= "Maize optimized sequence encoding VIP1A(a) with the Bacillus secretion signal removed as contained in pCIB5526"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| GATCCACC ATG AAG ACC AAC CAG ATC AGC ACC ACC CAG AAG AAC CAG CAG | 50  |
| Met Lys Thr Asn Gln Ile Ser Thr Thr Gln Lys Asn Gln Gln          |     |
| 825 830 835                                                      |     |
| AAG GAG ATG GAC CGC AAG GGC CTG CTG GGC TAC TAC TTC AAG GGC AAG  | 98  |
| Lys Glu Met Asp Arg Lys Gly Leu Leu Gly Tyr Tyr Phe Lys Gly Lys  |     |
| 840 845 850                                                      |     |
| GAC TTC AGC AAC CTG ACC ATG TTC GCC CCC ACG CGT GAC AGC ACC CTG  | 146 |
| Asp Phe Ser Asn Leu Thr Met Phe Ala Pro Thr Arg Asp Ser Thr Leu  |     |
| 855 860 865                                                      |     |
| ATC TAC GAC CAG CAG ACC GCC AAC AAG CTG CTG GAC AAG AAG CAG CAG  | 194 |
| Ile Tyr Asp Gln Gln Thr Ala Asn Lys Leu Leu Asp Lys Lys Gln Gln  |     |
| 870 875 880                                                      |     |
| GAG TAC CAG AGC ATC CGC TGG ATC GGC CTG ATC CAG AGC AAG GAG ACC  | 242 |
| Glu Tyr Gln Ser Ile Arg Trp Ile Gly Leu Ile Gln Ser Lys Glu Thr  |     |
| 885 890 895                                                      |     |
| GGC GAC TTC ACC TTC AAC CTG AGC GAG GAC GAG CAG GCC ATC ATC GAG  | 290 |
| Gly Asp Phe Thr Phe Asn Leu Ser Glu Asp Glu Gln Ala Ile Ile Glu  |     |
| 900 905 910 915                                                  |     |
| ATC AAC GGC AAG ATC ATC AGC AAC AAG GGC AAG GAG AAG CAG GTG GTG  | 338 |
| Ile Asn Gly Lys Ile Ile Ser Asn Lys Gly Lys Glu Lys Gln Val Val  |     |
| 920 925 930                                                      |     |
| CAC CTG GAG AAG GGC AAG CTG GTG CCC ATC AAG ATC GAG TAC CAG AGC  | 386 |

- 106 -

|                                                                 |      |
|-----------------------------------------------------------------|------|
| His Leu Glu Lys Gly Lys Leu Val Pro Ile Lys Ile Glu Tyr Gln Ser |      |
| 935 940 945                                                     |      |
| GAC ACC AAG TTC AAC ATC GAC AGC AAG ACC TTC AAG GAG CTG AAG CTT | 434  |
| Asp Thr Lys Phe Asn Ile Asp Ser Lys Thr Phe Lys Glu Leu Lys Leu |      |
| 950 955 960                                                     |      |
| TTC AAG ATC GAC AGC CAG AAC CAG CCC CAG CAG GTG CAG CAG GAC GAG | 482  |
| Phe Lys Ile Asp Ser Gln Asn Gln Pro Gln Gln Val Gln Gln Asp Glu |      |
| 965 970 975                                                     |      |
| CTG CGC AAC CCC GAG TTC AAC AAG AAG GAG AGC CAG GAG TTC CTG GCC | 530  |
| Leu Arg Asn Pro Glu Phe Asn Lys Lys Glu Ser Gln Glu Phe Leu Ala |      |
| 980 985 990 995                                                 |      |
| AAG CCC AGC AAG ATC AAC CTG TTC ACC CAG CAG ATG AAG CGC GAG ATC | 578  |
| Lys Pro Ser Lys Ile Asn Leu Phe Thr Gln Gln Met Lys Arg Glu Ile |      |
| 1000 1005 1010                                                  |      |
| GAC GAG GAC ACC GAC ACC GAC GGC GAC AGC ATC CCC GAC CTG TGG GAG | 626  |
| Asp Glu Asp Thr Asp Thr Asp Gly Asp Ser Ile Pro Asp Leu Trp Glu |      |
| 1015 1020 1025                                                  |      |
| GAG AAC GGC TAC ACC ATC CAG AAC CGC ATC GCC GTG AAG TGG GAC GAC | 674  |
| Glu Asn Gly Tyr Thr Ile Gln Asn Arg Ile Ala Val Lys Trp Asp Asp |      |
| 1030 1035 1040                                                  |      |
| AGC CTG GCT AGC AAG GGC TAC ACC AAG TTC GTG AGC AAC CCC CTG GAG | 722  |
| Ser Leu Ala Ser Lys Gly Tyr Thr Lys Phe Val Ser Asn Pro Leu Glu |      |
| 1045 1050 1055                                                  |      |
| AGC CAC ACC GTG GGC GAC CCC TAC ACC GAC TAC GAG AAG GCC GCC CGC | 770  |
| Ser His Thr Val Gly Asp Pro Tyr Thr Asp Tyr Glu Lys Ala Ala Arg |      |
| 1060 1065 1070 1075                                             |      |
| GAC CTG GAC CTG AGC AAC GCC AAG GAG ACC TTC AAC CCC CTG GTG GCC | 818  |
| Asp Leu Asp Leu Ser Asn Ala Lys Glu Thr Phe Asn Pro Leu Val Ala |      |
| 1080 1085 1090                                                  |      |
| GCC TTC CCC AGC GTG AAC GTG AGC ATG GAG AAG GTG ATC CTG AGC CCC | 866  |
| Ala Phe Pro Ser Val Asn Val Ser Met Glu Lys Val Ile Leu Ser Pro |      |
| 1095 1100 1105                                                  |      |
| AAC GAG AAC CTG AGC AAC AGC GTG GAG AGC CAC TCG AGC ACC AAC TGG | 914  |
| Asn Glu Asn Leu Ser Asn Ser Val Glu Ser His Ser Ser Thr Asn Trp |      |
| 1110 1115 1120                                                  |      |
| AGC TAC ACC AAC ACC GAG GGC GCC AGC GTG GAG GCC GGC ATC GGT CCC | 962  |
| Ser Tyr Thr Asn Thr Glu Gly Ala Ser Val Glu Ala Gly Ile Gly Pro |      |
| 1125 1130 1135                                                  |      |
| AAG GGC ATC AGC TTC GGC GTG AGC GTG AAC TAC CAG CAC AGC GAG ACC | 1010 |
| Lys Gly Ile Ser Phe Gly Val Ser Val Asn Tyr Gln His Ser Glu Thr |      |
| 1140 1145 1150 1155                                             |      |



- 107 -

|                                                                                                                                                           |      |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| GTG GCC CAG GAG TGG GGC ACC AGC ACC GGC AAC ACC AGC CAG TTC AAC<br>Val Ala Gln Glu Trp Gly Thr Ser Thr Gly Asn Thr Ser Gln Phe Asn<br>1160 1165 1170      | 1058 |
| ACC GCC AGC GCC GGC TAC CTG AAC GCC AAC GTG CGC TAC AAC AAC GTG<br>Thr Ala Ser Ala Gly Tyr Leu Asn Ala Asn Val Arg Tyr Asn Asn Val<br>1175 1180 1185      | 1106 |
| GGC ACC GGC GCC ATC TAC GAC GTG AAG CCC ACC ACC AGC TTC GTG CTG<br>Gly Thr Gly Ala Ile Tyr Asp Val Lys Pro Thr Thr Ser Phe Val Leu<br>1190 1195 1200      | 1154 |
| AAC AAC GAC ACC ATC GCC ACC ATC ACC GCC AAG TCG AAT TCC ACC GCC<br>Asn Asn Asp Thr Ile Ala Thr Ile Thr Ala Lys Ser Asn Ser Thr Ala<br>1205 1210 1215      | 1202 |
| CTG AAC ATC AGC CCC GGC GAG AGC TAC CCC AAG AAG GGC CAG AAC GGC<br>Leu Asn Ile Ser Pro Gly Glu Ser Tyr Pro Lys Lys Gly Gln Asn Gly<br>1220 1225 1230 1235 | 1250 |
| ATC GCC ATC ACC AGC ATG GAC GAC TTC AAC AGC CAC CCC ATC ACC CTG<br>Ile Ala Ile Thr Ser Met Asp Asp Phe Asn Ser His Pro Ile Thr Leu<br>1240 1245 1250      | 1298 |
| AAC AAG AAG CAG GTG GAC AAC CTG CTG AAC AAC AAG CCC ATG ATG CTG<br>Asn Lys Lys Gln Val Asp Asn Leu Leu Asn Asn Lys Pro Met Met Leu<br>1255 1260 1265      | 1346 |
| GAG ACC AAC CAG ACC GAC GGC GTC TAC AAG ATC AAG GAC ACC CAC GGC<br>Glu Thr Asn Gln Thr Asp Gly Val Tyr Lys Ile Lys Asp Thr His Gly<br>1270 1275 1280      | 1394 |
| AAC ATC GTG ACG GGC GGC GAG TGG AAC GGC GTG ATC CAG CAG ATC AAG<br>Asn Ile Val Thr Gly Gly Glu Trp Asn Gly Val Ile Gln Gln Ile Lys<br>1285 1290 1295      | 1442 |
| GCC AAG ACC GCC AGC ATC ATC GTC GAC GAC GGC GAG CGC GTG GCC GAG<br>Ala Lys Thr Ala Ser Ile Ile Val Asp Asp Gly Glu Arg Val Ala Glu<br>1300 1305 1310 1315 | 1490 |
| AAG CGC GTG GCC GCC AAG GAC TAC GAG AAC CCC GAG GAC AAG ACC CCC<br>Lys Arg Val Ala Ala Lys Asp Tyr Glu Asn Pro Glu Asp Lys Thr Pro<br>1320 1325 1330      | 1538 |
| AGC CTG ACC CTG AAG GAC GCC CTG AAG CTG AGC TAC CCC GAC GAG ATC<br>Ser Leu Thr Leu Lys Asp Ala Leu Lys Leu Ser Tyr Pro Asp Glu Ile<br>1335 1340 1345      | 1586 |
| AAG GAG ATC GAG GGC TTG CTG TAC TAC AAG AAC AAG CCC ATC TAC GAG<br>Lys Glu Ile Glu Gly Leu Leu Tyr Tyr Lys Asn Lys Pro Ile Tyr Glu<br>1350 1355 1360      | 1634 |
| AGC AGC GTG ATG ACC TAT CTA GAC GAG AAC ACC GCC AAG GAG GTG ACC<br>Ser Ser Val Met Thr Tyr Leu Asp Glu Asn Thr Ala Lys Glu Val Thr<br>1365 1370 1375      | 1682 |

- 108 -

|                                                                                                                                                           |      |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| AAG CAG CTG AAC GAC ACC ACC GGC AAG TTC AAG GAC GTG AGC CAC CTG<br>Lys Gln Leu Asn Asp Thr Thr Gly Lys Phe Lys Asp Val Ser His Leu<br>1380 1385 1390 1395 | 1730 |
| TAC GAC GTG AAG CTG ACC CCC AAG ATG AAC GTG ACC ATC AAG CTG AGC<br>Tyr Asp Val Lys Leu Thr Pro Lys Met Asn Val Thr Ile Lys Leu Ser<br>1400 1405 1410      | 1778 |
| ATC CTG TAC GAC AAC GCC GAG AGC AAC GAC AAC AGC ATC GGC AAG TGG<br>Ile Leu Tyr Asp Asn Ala Glu Ser Asn Asp Asn Ser Ile Gly Lys Trp<br>1415 1420 1425      | 1826 |
| ACC AAC ACC AAC ATC GTG AGC GGC GGC AAC AAC GGC AAG AAG CAG TAC<br>Thr Asn Thr Asn Ile Val Ser Gly Gly Asn Asn Gly Lys Lys Gln Tyr<br>1430 1435 1440      | 1874 |
| AGC AGC AAC AAC CCC GAC GCC AAC CTG ACC CTG AAC ACC GAC GCC CAG<br>Ser Ser Asn Asn Pro Asp Ala Asn Leu Thr Leu Asn Thr Asp Ala Gln<br>1445 1450 1455      | 1922 |
| GAG AAG CTG AAC AAG AAC CGC GAC TAC TAC ATC AGC CTG TAC ATG AAG<br>Glu Lys Leu Asn Lys Asn Arg Asp Tyr Tyr Ile Ser Leu Tyr Met Lys<br>1460 1465 1470 1475 | 1970 |
| AGC GAG AAG AAC ACC CAG TGC GAG ATC ACC ATC GAC GGC GAG ATA TAC<br>Ser Glu Lys Asn Thr Gln Cys Glu Ile Thr Ile Asp Gly Glu Ile Tyr<br>1480 1485 1490      | 2018 |
| CCC ATC ACC ACC AAG ACC GTG AAC GTG AAC AAG GAC AAC TAC AAG CGC<br>Pro Ile Thr Thr Lys Thr Val Asn Val Asn Lys Asp Asn Tyr Lys Arg<br>1495 1500 1505      | 2066 |
| CTG GAC ATC ATC GCC CAC AAC ATC AAG AGC AAC CCC ATC AGC AGC CTG<br>Leu Asp Ile Ile Ala His Asn Ile Lys Ser Asn Pro Ile Ser Ser Leu<br>1510 1515 1520      | 2114 |
| CAC ATC AAG ACC AAC GAC GAG ATC ACC CTG TTC TGG GAC GAC ATA TCG<br>His Ile Lys Thr Asn Asp Glu Ile Thr Leu Phe Trp Asp Asp Ile Ser<br>1525 1530 1535      | 2162 |
| ATT ACC GAC GTC GCC AGC ATC AAG CCC GAG AAC CTG ACC GAC AGC GAG<br>Ile Thr Asp Val Ala Ser Ile Lys Pro Glu Asn Leu Thr Asp Ser Glu<br>1540 1545 1550 1555 | 2210 |
| ATC AAG CAG ATA TAC AGT CGC TAC GGC ATC AAG CTG GAG GAC GGC ATC<br>Ile Lys Gln Ile Tyr Ser Arg Tyr Gly Ile Lys Leu Glu Asp Gly Ile<br>1560 1565 1570      | 2258 |
| CTG ATC GAC AAG AAA GGC GGC ATC CAC TAC GGC GAG TTC ATC AAC GAG<br>Leu Ile Asp Lys Lys Gly Gly Ile His Tyr Gly Glu Phe Ile Asn Glu<br>1575 1580 1585      | 2306 |
| GCC AGC TTC AAC ATC GAG CCC CTG CAG AAC TAC GTG ACC AAG TAC GAG<br>Ala Ser Phe Asn Ile Glu Pro Leu Gln Asn Tyr Val Thr Lys Tyr Glu                        | 2354 |

- 109 -

| 1590                                                            | 1595 | 1600 |      |
|-----------------------------------------------------------------|------|------|------|
| GTG ACC TAC AGC AGC GAG CTG GGC CCC AAC GTG AGC GAC ACC CTG GAG |      |      | 2402 |
| Val Thr Tyr Ser Ser Glu Leu Gly Pro Asn Val Ser Asp Thr Leu Glu |      |      |      |
| 1605                                                            | 1610 | 1615 |      |
| AGC GAC AAG ATT TAC AAG GAC GGC ACC ATC AAG TTC GAC TTC ACC AAG |      |      | 2450 |
| Ser Asp Lys Ile Tyr Lys Asp Gly Thr Ile Lys Phe Asp Phe Thr Lys |      |      |      |
| 1620                                                            | 1625 | 1630 | 1635 |
| TAC AGC AAG AAC GAG CAG GGC CTG TTC TAC GAC AGC GGC CTG AAC TGG |      |      | 2498 |
| Tyr Ser Lys Asn Glu Gln Gly Leu Phe Tyr Asp Ser Gly Leu Asn Trp |      |      |      |
|                                                                 | 1640 | 1645 | 1650 |
| GAC TTC AAG ATC AAC GCC ATC ACC TAC GAC GGC AAG GAG ATG AAC GTG |      |      | 2546 |
| Asp Phe Lys Ile Asn Ala Ile Thr Tyr Asp Gly Lys Glu Met Asn Val |      |      |      |
|                                                                 | 1655 | 1660 | 1665 |
| TTC CAC CGC TAC AAC AAG TAGATCTGAG CT                           |      |      | 2576 |
| Phe His Arg Tyr Asn Lys                                         |      |      |      |
| 1670                                                            |      |      |      |

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Thr | Asn | Gln | Ile | Ser | Thr | Thr | Gln | Lys | Asn | Gln | Gln | Lys | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Asp | Arg | Lys | Gly | Leu | Leu | Gly | Tyr | Tyr | Phe | Lys | Gly | Lys | Asp | Phe |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ser | Asn | Leu | Thr | Met | Phe | Ala | Pro | Thr | Arg | Asp | Ser | Thr | Leu | Ile | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Gln | Gln | Thr | Ala | Asn | Lys | Leu | Leu | Asp | Lys | Lys | Gln | Gln | Glu | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Ser | Ile | Arg | Trp | Ile | Gly | Leu | Ile | Gln | Ser | Lys | Glu | Thr | Gly | Asp |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Phe | Thr | Phe | Asn | Leu | Ser | Glu | Asp | Glu | Gln | Ala | Ile | Ile | Glu | Ile | Asn |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Lys | Ile | Ile | Ser | Asn | Lys | Gly | Lys | Glu | Lys | Gln | Val | Val | His | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |

- 110 -

Glu Lys Gly Lys Leu Val Pro Ile Lys Ile Glu Tyr Gln Ser Asp Thr  
 115 120 125  
 Lys Phe Asn Ile Asp Ser Lys Thr Phe Lys Glu Leu Lys Leu Phe Lys  
 130 135 140  
 Ile Asp Ser Gln Asn Gln Pro Gln Gln Val Gln Gln Asp Glu Leu Arg  
 145 150 155 160  
 Asn Pro Glu Phe Asn Lys Lys Glu Ser Gln Glu Phe Leu Ala Lys Pro  
 165 170 175  
 Ser Lys Ile Asn Leu Phe Thr Gln Gln Met Lys Arg Glu Ile Asp Glu  
 180 185 190  
 Asp Thr Asp Thr Asp Gly Asp Ser Ile Pro Asp Leu Trp Glu Glu Asn  
 195 200 205  
 Gly Tyr Thr Ile Gln Asn Arg Ile Ala Val Lys Trp Asp Asp Ser Leu  
 210 215 220  
 Ala Ser Lys Gly Tyr Thr Lys Phe Val Ser Asn Pro Leu Glu Ser His  
 225 230 235 240  
 Thr Val Gly Asp Pro Tyr Thr Asp Tyr Glu Lys Ala Ala Arg Asp Leu  
 245 250 255  
 Asp Leu Ser Asn Ala Lys Glu Thr Phe Asn Pro Leu Val Ala Ala Phe  
 260 265 270  
 Pro Ser Val Asn Val Ser Met Glu Lys Val Ile Leu Ser Pro Asn Glu  
 275 280 285  
 Asn Leu Ser Asn Ser Val Glu Ser His Ser Ser Thr Asn Trp Ser Tyr  
 290 295 300  
 Thr Asn Thr Glu Gly Ala Ser Val Glu Ala Gly Ile Gly Pro Lys Gly  
 305 310 315 320  
 Ile Ser Phe Gly Val Ser Val Asn Tyr Gln His Ser Glu Thr Val Ala  
 325 330 335  
 Gln Glu Trp Gly Thr Ser Thr Gly Asn Thr Ser Gln Phe Asn Thr Ala  
 340 345 350  
 Ser Ala Gly Tyr Leu Asn Ala Asn Val Arg Tyr Asn Asn Val Gly Thr  
 355 360 365  
 Gly Ala Ile Tyr Asp Val Lys Pro Thr Thr Ser Phe Val Leu Asn Asn  
 370 375 380  
 Asp Thr Ile Ala Thr Ile Thr Ala Lys Ser Asn Ser Thr Ala Leu Asn  
 385 390 395 400  
 Ile Ser Pro Gly Glu Ser Tyr Pro Lys Lys Gly Gln Asn Gly Ile Ala

- 111 -

|                                                                 |     |         |
|-----------------------------------------------------------------|-----|---------|
| 405                                                             | 410 | 415     |
| Ile Thr Ser Met Asp Asp Phe Asn Ser His Pro Ile Thr Leu Asn Lys |     |         |
| 420                                                             | 425 | 430     |
| Lys Gln Val Asp Asn Leu Leu Asn Asn Lys Pro Met Met Leu Glu Thr |     |         |
| 435                                                             | 440 | 445     |
| Asn Gln Thr Asp Gly Val Tyr Lys Ile Lys Asp Thr His Gly Asn Ile |     |         |
| 450                                                             | 455 | 460     |
| Val Thr Gly Gly Glu Trp Asn Gly Val Ile Gln Gln Ile Lys Ala Lys |     |         |
| 465                                                             | 470 | 475 480 |
| Thr Ala Ser Ile Ile Val Asp Asp Gly Glu Arg Val Ala Glu Lys Arg |     |         |
| 485                                                             | 490 | 495     |
| Val Ala Ala Lys Asp Tyr Glu Asn Pro Glu Asp Lys Thr Pro Ser Leu |     |         |
| 500                                                             | 505 | 510     |
| Thr Leu Lys Asp Ala Leu Lys Leu Ser Tyr Pro Asp Glu Ile Lys Glu |     |         |
| 515                                                             | 520 | 525     |
| Ile Glu Gly Leu Leu Tyr Tyr Lys Asn Lys Pro Ile Tyr Glu Ser Ser |     |         |
| 530                                                             | 535 | 540     |
| Val Met Thr Tyr Leu Asp Glu Asn Thr Ala Lys Glu Val Thr Lys Gln |     |         |
| 545                                                             | 550 | 555 560 |
| Leu Asn Asp Thr Thr Gly Lys Phe Lys Asp Val Ser His Leu Tyr Asp |     |         |
| 565                                                             | 570 | 575     |
| Val Lys Leu Thr Pro Lys Met Asn Val Thr Ile Lys Leu Ser Ile Leu |     |         |
| 580                                                             | 585 | 590     |
| Tyr Asp Asn Ala Glu Ser Asn Asp Asn Ser Ile Gly Lys Trp Thr Asn |     |         |
| 595                                                             | 600 | 605     |
| Thr Asn Ile Val Ser Gly Gly Asn Asn Gly Lys Lys Gln Tyr Ser Ser |     |         |
| 610                                                             | 615 | 620     |
| Asn Asn Pro Asp Ala Asn Leu Thr Leu Asn Thr Asp Ala Gln Glu Lys |     |         |
| 625                                                             | 630 | 635 640 |
| Leu Asn Lys Asn Arg Asp Tyr Tyr Ile Ser Leu Tyr Met Lys Ser Glu |     |         |
| 645                                                             | 650 | 655     |
| Lys Asn Thr Gln Cys Glu Ile Thr Ile Asp Gly Glu Ile Tyr Pro Ile |     |         |
| 660                                                             | 665 | 670     |
| Thr Thr Lys Thr Val Asn Val Asn Lys Asp Asn Tyr Lys Arg Leu Asp |     |         |
| 675                                                             | 680 | 685     |
| Ile Ile Ala His Asn Ile Lys Ser Asn Pro Ile Ser Ser Leu His Ile |     |         |
| 690                                                             | 695 | 700     |

- 112 -

Lys Thr Asn Asp Glu Ile Thr Leu Phe Trp Asp Asp Ile Ser Ile Thr  
 705 710 715 720  
 Asp Val Ala Ser Ile Lys Pro Glu Asn Leu Thr Asp Ser Glu Ile Lys  
 725 730 735  
 Gln Ile Tyr Ser Arg Tyr Gly Ile Lys Leu Glu Asp Gly Ile Leu Ile  
 740 745 750  
 Asp Lys Lys Gly Gly Ile His Tyr Gly Glu Phe Ile Asn Glu Ala Ser  
 755 760 765  
 Phe Asn Ile Glu Pro Leu Gln Asn Tyr Val Thr Lys Tyr Glu Val Thr  
 770 775 780  
 Tyr Ser Ser Glu Leu Gly Pro Asn Val Ser Asp Thr Leu Glu Ser Asp  
 785 790 795 800  
 Lys Ile Tyr Lys Asp Gly Thr Ile Lys Phe Asp Phe Thr Lys Tyr Ser  
 805 810 815  
 Lys Asn Glu Gln Gly Leu Phe Tyr Asp Ser Gly Leu Asn Trp Asp Phe  
 820 825 830  
 Lys Ile Asn Ala Ile Thr Tyr Asp Gly Lys Glu Met Asn Val Phe His  
 835 840 845  
 Arg Tyr Asn Lys  
 850

## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "forward primer used to make pCIB5527"

## (iii) HYPOTHETICAL: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGATCCACCA TGCTGCAGAA CCTGAAGATC AC

32

## (2) INFORMATION FOR SEQ ID NO:38:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "reverse primer used to make pCIB5527"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AAGCTTCCAC TCCTTCTC

18

(2) INFORMATION FOR SEO ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1241 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 9..1238

(D) OTHER INFORMATION: /note= "Maize optimized DNA sequence encoding VIP2A(a) with the Bacillus secretion signal removed as contained in pCIB5527"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GATCCACC ATG CTG CAG AAC CTG AAG ATC ACC GAC AAG GTG GAG GAC TTC 50  
Met Leu Gln Asn Leu Lys Ile Thr Asp Lys Val Glu Asp Phe  
855 860 865

AAG GAG GAC AAG GAG AAG GCC AAG GAG TGG GGC AAG GAG AAG GAG AAG  
Lys Glu Asp Lys Glu Lys Ala Lys Glu Trp Gly Lys Glu Lys Glu Lys 98  
870 875 880

GAG TGG AAG CTT ACC GCC ACC GAG AAG GGC AAG ATG AAC AAC TTC CTG 146  
Glu Trp Lys Leu Thr Ala Thr Glu Lys Gly Lys Met Asn Asn Phe Leu  
885 890 895

GAC AAC AAG AAC GAC ATC AAG ACC AAC TAC AAG GAG ATC ACC TTC AGC 194

- 114 -

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Asp Asn Lys Asn Asp Ile Lys Thr Asn Tyr Lys Glu Ile Thr Phe Ser |     |
| 900 905 910                                                     |     |
| ATA GCC GGC AGC TTC GAG GAC GAG ATC AAG GAC CTG AAG GAG ATC GAC | 242 |
| Ile Ala Gly Ser Phe Glu Asp Glu Ile Lys Asp Leu Lys Glu Ile Asp |     |
| 915 920 925 930                                                 |     |
| AAG ATG TTC GAC AAG ACC AAC CTG AGC AAC AGC ATC ATC ACC TAC AAG | 290 |
| Lys Met Phe Asp Lys Thr Asn Leu Ser Asn Ser Ile Ile Thr Tyr Lys |     |
| 935 940 945                                                     |     |
| AAC GTG GAG CCC ACC ACC ATC GGC TTC AAC AAG AGC CTG ACC GAG GGC | 338 |
| Asn Val Glu Pro Thr Thr Ile Gly Phe Asn Lys Ser Leu Thr Glu Gly |     |
| 950 955 960                                                     |     |
| AAC ACC ATC AAC AGC GAC GCC ATG GCC CAG TTC AAG GAG CAG TTC CTG | 386 |
| Asn Thr Ile Asn Ser Asp Ala Met Ala Gln Phe Lys Glu Gln Phe Leu |     |
| 965 970 975                                                     |     |
| GAC CGC GAC ATC AAG TTC GAC AGC TAC CTG GAC ACC CAC CTG ACC GCC | 434 |
| Asp Arg Asp Ile Lys Phe Asp Ser Tyr Leu Asp Thr His Leu Thr Ala |     |
| 980 985 990                                                     |     |
| CAG CAG GTG AGC AGC AAG GAG CGC GTG ATC CTG AAG GTG ACC GTC CCC | 482 |
| Gln Gln Val Ser Ser Lys Glu Arg Val Ile Leu Lys Val Thr Val Pro |     |
| 995 1000 1005 1010                                              |     |
| AGC GGC AAG GGC AGC ACC ACC CCC ACC AAG GCC GGC GTG ATC CTG AAC | 530 |
| Ser Gly Lys Gly Ser Thr Thr Pro Thr Lys Ala Gly Val Ile Leu Asn |     |
| 1015 1020 1025                                                  |     |
| AAC AGC GAG TAC AAG ATG CTG ATC GAC AAC GGC TAC ATG GTG CAC GTG | 578 |
| Asn Ser Glu Tyr Lys Met Leu Ile Asp Asn Gly Tyr Met Val His Val |     |
| 1030 1035 1040                                                  |     |
| GAC AAG GTG AGC AAG GTG GTG AAG AAG GGC GTG GAG TGC CTC CAG ATC | 626 |
| Asp Lys Val Ser Lys Val Val Lys Lys Gly Val Glu Cys Leu Gln Ile |     |
| 1045 1050 1055                                                  |     |
| GAG GGC ACC CTG AAG AAG AGT CTA GAC TTC AAG AAC GAC ATC AAC GCC | 674 |
| Glu Gly Thr Leu Lys Lys Ser Leu Asp Phe Lys Asn Asp Ile Asn Ala |     |
| 1060 1065 1070                                                  |     |
| GAG GCC CAC AGC TGG GGC ATG AAG AAC TAC GAG GAG TGG GCC AAG GAC | 722 |
| Glu Ala His Ser Trp Gly Met Lys Asn Tyr Glu Glu Trp Ala Lys Asp |     |
| 1075 1080 1085 1090                                             |     |
| CTG ACC GAC AGC CAG CGC GAG GCC CTG GAC GGC TAC GCC CGC CAG GAC | 770 |
| Leu Thr Asp Ser Gln Arg Glu Ala Leu Asp Gly Tyr Ala Arg Gln Asp |     |
| 1095 1100 1105                                                  |     |
| TAC AAG GAG ATC AAC AAC TAC CTG CGC AAC CAG GGC GGC AGC GGC AAC | 818 |
| Tyr Lys Glu Ile Asn Asn Tyr Leu Arg Asn Gln Gly Gly Ser Gly Asn |     |
| 1110 1115 1120                                                  |     |



- 115 -

|                                                                                                                                                           |      |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| GAG AAG CTG GAC GCC CAG ATC AAG AAC ATC AGC GAC GCC CTG GGC AAG<br>Glu Lys Leu Asp Ala Gln Ile Lys Asn Ile Ser Asp Ala Leu Gly Lys<br>1125 1130 1135      | 866  |
| AAG CCC ATC CCC GAG AAC ATC ACC GTG TAC CGC TGG TGC GGC ATG CCC<br>Lys Pro Ile Pro Glu Asn Ile Thr Val Tyr Arg Trp Cys Gly Met Pro<br>1140 1145 1150      | 914  |
| GAG TTC GGC TAC CAG ATC AGC GAC CCC CTG CCC AGC CTG AAG GAC TTC<br>Glu Phe Gly Tyr Gln Ile Ser Asp Pro Leu Pro Ser Leu Lys Asp Phe<br>1155 1160 1165 1170 | 962  |
| GAG GAG CAG TTC CTG-AAC ACC ATC AAG GAG GAC AAG GGC TAC ATG AGC<br>Glu Glu Gln Phe Leu Asn Thr Ile Lys Glu Asp Lys Gly Tyr Met Ser<br>1175 1180 1185      | 1010 |
| ACC AGC CTG AGC AGC GAG CGC CTG GCC GCC TTC GGC AGC CGC AAG ATC<br>Thr Ser Leu Ser Ser Glu Arg Leu Ala Ala Phe Gly Ser Arg Lys Ile<br>1190 1195 1200      | 1058 |
| ATC CTG CGC CTG CAG GTG CCC AAG GGC AGC ACT GGT GCC TAC CTG AGC<br>Ile Leu Arg Leu Gln Val Pro Lys Gly Ser Thr Gly Ala Tyr Leu Ser<br>1205 1210 1215      | 1106 |
| GCC ATC GGC GGC TTC GCC AGC GAG AAG GAG ATC CTG CTG GAT AAG GAC<br>Ala Ile Gly Gly Phe Ala Ser Glu Lys Glu Ile Leu Leu Asp Lys Asp<br>1220 1225 1230      | 1154 |
| AGC AAG TAC CAC ATC GAC AAG GTG ACC GAG GTG ATC ATC AAG GGC GTG<br>Ser Lys Tyr His Ile Asp Lys Val Thr Glu Val Ile Ile Lys Gly Val<br>1235 1240 1245 1250 | 1202 |
| AAG CGC TAC GTG GTG GAC GCC ACC CTG CTG ACC AAC TAG<br>Lys Arg Tyr Val Val Asp Ala Thr Leu Leu Thr Asn<br>1255 1260                                       | 1241 |

## (2) INFORMATION FOR SEQ ID NO:40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gln | Asn | Leu | Lys | Ile | Thr | Asp | Lys | Val | Glu | Asp | Phe | Lys | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Lys | Glu | Lys | Ala | Lys | Glu | Trp | Gly | Lys | Glu | Lys | Glu | Lys | Glu | Trp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Lys | Leu | Thr | Ala | Thr | Glu | Lys | Gly | Lys | Met | Asn | Asn | Phe | Leu | Asp | Asn |

- 116 -

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 35                                                              | 40  | 45  |
| Lys Asn Asp Ile Lys Thr Asn Tyr Lys Glu Ile Thr Phe Ser Ile Ala |     |     |
| 50                                                              | 55  | 60  |
| Gly Ser Phe Glu Asp Glu Ile Lys Asp Leu Lys Glu Ile Asp Lys Met |     |     |
| 65                                                              | 70  | 75  |
| Phe Asp Lys Thr Asn Leu Ser Asn Ser Ile Ile Thr Tyr Lys Asn Val |     |     |
|                                                                 | 85  | 90  |
| Glu Pro Thr Thr Ile Gly Phe Asn Lys Ser Leu Thr Glu Gly Asn Thr |     |     |
|                                                                 | 100 | 105 |
| Ile Asn Ser Asp Ala Met Ala Gln Phe Lys Glu Gln Phe Leu Asp Arg |     |     |
|                                                                 | 115 | 120 |
| Asp Ile Lys Phe Asp Ser Tyr Leu Asp Thr His Leu Thr Ala Gln Gln |     |     |
|                                                                 | 130 | 135 |
| Val Ser Ser Lys Glu Arg Val Ile Leu Lys Val Thr Val Pro Ser Gly |     |     |
|                                                                 | 145 | 150 |
| Lys Gly Ser Thr Thr Pro Thr Lys Ala Gly Val Ile Leu Asn Asn Ser |     |     |
|                                                                 | 165 | 170 |
| Glu Tyr Lys Met Leu Ile Asp Asn Gly Tyr Met Val His Val Asp Lys |     |     |
|                                                                 | 180 | 185 |
| Val Ser Lys Val Val Lys Lys Gly Val Glu Cys Leu Gln Ile Glu Gly |     |     |
|                                                                 | 195 | 200 |
| Thr Leu Lys Lys Ser Leu Asp Phe Lys Asn Asp Ile Asn Ala Glu Ala |     |     |
|                                                                 | 210 | 215 |
| His Ser Trp Gly Met Lys Asn Tyr Glu Glu Trp Ala Lys Asp Leu Thr |     |     |
|                                                                 | 225 | 230 |
| Asp Ser Gln Arg Glu Ala Leu Asp Gly Tyr Ala Arg Gln Asp Tyr Lys |     |     |
|                                                                 | 245 | 250 |
| Glu Ile Asn Asn Tyr Leu Arg Asn Gln Gly Gly Ser Gly Asn Glu Lys |     |     |
|                                                                 | 260 | 265 |
| Leu Asp Ala Gln Ile Lys Asn Ile Ser Asp Ala Leu Gly Lys Lys Pro |     |     |
|                                                                 | 275 | 280 |
| Ile Pro Glu Asn Ile Thr Val Tyr Arg Trp Cys Gly Met Pro Glu Phe |     |     |
|                                                                 | 290 | 295 |
| Gly Tyr Gln Ile Ser Asp Pro Leu Pro Ser Leu Lys Asp Phe Glu Glu |     |     |
|                                                                 | 305 | 310 |
| Gln Phe Leu Asn Thr Ile Lys Glu Asp Lys Gly Tyr Met Ser Thr Ser |     |     |
|                                                                 | 325 | 330 |
|                                                                 |     | 335 |

- 117 -

Leu Ser Ser Glu Arg Leu Ala Ala Phe Gly Ser Arg Lys Ile Ile Leu  
                   340                                  345                                  350  
 Arg Leu Gln Val Pro Lys Gly Ser Thr Gly Ala Tyr Leu Ser Ala Ile  
                   355                                  360                                  365  
 Gly Gly Phe Ala Ser Glu Lys Glu Ile Leu Leu Asp Lys Asp Ser Lys  
                   370                                  375                                  380  
 Tyr His Ile Asp Lys Val Thr Glu Val Ile Ile Lys Gly Val Lys Arg  
 385                                  390                                  395                                  400  
 Tyr Val Val Asp Ala Thr Leu Leu Thr Asn  
                                   405                                  410

## (2) INFORMATION FOR SEQ ID NO:41:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide encoding eukaryotic secretion signal used to construct pCIB5527"

## (iii) HYPOTHETICAL: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGATCCACCA TGGGCTGGAG CTGGATCTTC CTGTTCTGTC TGAGCGGCGC CGCGGGCGTG      60  
 CACTGCCTGC AG      72

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA"

## (iii) HYPOTHETICAL: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS

- 118 -

(B) LOCATION: 9..1238

(D) OTHER INFORMATION: /note= "Maize optimized DNA sequence encoding VIP2A(a) with the Bacillus secretion signal removed and the eukaryotic secretion signal inserted as contained in pCIB5528"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| GATCCACC ATG CTG CAG AAC CTG AAG ATC ACC GAC AAG GTG GAG GAC TTC | 50  |
| Met Leu Gln Asn Leu Lys Ile Thr Asp Lys Val Glu Asp Phe          |     |
| 415 420                                                          |     |
| AAG GAG GAC AAG GAG AAG GCC AAG GAG TGG GGC AAG GAG AAG GAG AAG  | 98  |
| Lys Glu Asp Lys Glu Lys Ala Lys Glu Trp Gly Lys Glu Lys Glu Lys  |     |
| 425 430 435 440                                                  |     |
| GAG TGG AAG CTT ACC GCC ACC GAG AAG GGC AAG ATG AAC AAC TTC CTG  | 146 |
| Glu Trp Lys Leu Thr Ala Thr Glu Lys Gly Lys Met Asn Asn Phe Leu  |     |
| 445 450 455                                                      |     |
| GAC AAC AAG AAC GAC ATC AAG ACC AAC TAC AAG GAG ATC ACC TTC AGC  | 194 |
| Asp Asn Lys Asn Asp Ile Lys Thr Asn Tyr Lys Glu Ile Thr Phe Ser  |     |
| 460 465 470                                                      |     |
| ATA GCC GGC AGC TTC GAG GAC GAG ATC AAG GAC CTG AAG GAG ATC GAC  | 242 |
| Ile Ala Gly Ser Phe Glu Asp Glu Ile Lys Asp Leu Lys Glu Ile Asp  |     |
| 475 480 485                                                      |     |
| AAG ATG TTC GAC AAG ACC AAC CTG AGC AAC AGC ATC ATC ACC TAC AAG  | 290 |
| Lys Met Phe Asp Lys Thr Asn Leu Ser Asn Ser Ile Ile Thr Tyr Lys  |     |
| 490 495 500                                                      |     |
| AAC GTG GAG CCC ACC ACC ATC GGC TTC AAC AAG AGC CTG ACC GAG GGC  | 338 |
| Asn Val Glu Pro Thr Thr Ile Gly Phe Asn Lys Ser Leu Thr Glu Gly  |     |
| 505 510 515 520                                                  |     |
| AAC ACC ATC AAC AGC GAC GCC ATG GCC CAG TTC AAG GAG CAG TTC CTG  | 386 |
| Asn Thr Ile Asn Ser Asp Ala Met Ala Gln Phe Lys Glu Gln Phe Leu  |     |
| 525 530 535                                                      |     |
| GAC CGC GAC ATC AAG TTC GAC AGC TAC CTG GAC ACC CAC CTG ACC GCC  | 434 |
| Asp Arg Asp Ile Lys Phe Asp Ser Tyr Leu Asp Thr His Leu Thr Ala  |     |
| 540 545 550                                                      |     |
| CAG CAG GTG AGC AGC AAG GAG CGC GTG ATC CTG AAG GTG ACC GTC CCC  | 482 |
| Gln Gln Val Ser Ser Lys Glu Arg Val Ile Leu Lys Val Thr Val Pro  |     |
| 555 560 565                                                      |     |
| AGC GGC AAG GGC AGC ACC ACC CCC ACC AAG GCC GGC GTG ATC CTG AAC  | 530 |
| Ser Gly Lys Gly Ser Thr Pro Thr Lys Ala Gly Val Ile Leu Asn      |     |
| 570 575 580                                                      |     |
| AAC AGC GAG TAC AAG ATG CTG ATC GAC AAC GGC TAC ATG GTG CAC GTG  | 578 |
| Asn Ser Glu Tyr Lys Met Leu Ile Asp Asn Gly Tyr Met Val His Val  |     |

- 119 -

|                                                                 |     |     |  |     |  |     |      |
|-----------------------------------------------------------------|-----|-----|--|-----|--|-----|------|
| 585                                                             |     | 590 |  | 595 |  | 600 |      |
| GAC AAG GTG AGC AAG GTG GTG AAG AAG GGC GTG GAG TGC CTC CAG ATC |     |     |  |     |  |     | 626  |
| Asp Lys Val Ser Lys Val Val Lys Lys Gly Val Glu Cys Leu Gln Ile |     |     |  |     |  |     |      |
|                                                                 | 605 |     |  | 610 |  | 615 |      |
| GAG GGC ACC CTG AAG AAG AGT CTA GAC TTC AAG AAC GAC ATC AAC GCC |     |     |  |     |  |     | 674  |
| Glu Gly Thr Leu Lys Lys Ser Leu Asp Phe Lys Asn Asp Ile Asn Ala |     |     |  |     |  |     |      |
|                                                                 | 620 |     |  | 625 |  | 630 |      |
| GAG GCC CAC AGC TGG GGC ATG AAG AAC TAC GAG GAG TGG GCC AAG GAC |     |     |  |     |  |     | 722  |
| Glu Ala His Ser Trp Gly Met Lys Asn Tyr Glu Glu Trp Ala Lys Asp |     |     |  |     |  |     |      |
|                                                                 | 635 |     |  | 640 |  | 645 |      |
| CTG ACC GAC AGC CAG CGC GAG GCC CTG GAC GGC TAC GCC CGC CAG GAC |     |     |  |     |  |     | 770  |
| Leu Thr Asp Ser Gln Arg Glu Ala Leu Asp Gly Tyr Ala Arg Gln Asp |     |     |  |     |  |     |      |
|                                                                 | 650 |     |  | 655 |  | 660 |      |
| TAC AAG GAG ATC AAC AAC TAC CTG CGC AAC CAG GGC GGC AGC GGC AAC |     |     |  |     |  |     | 818  |
| Tyr Lys Glu Ile Asn Asn Tyr Leu Arg Asn Gln Gly Gly Ser Gly Asn |     |     |  |     |  |     |      |
|                                                                 | 665 |     |  | 670 |  | 675 | 680  |
| GAG AAG CTG GAC GCC CAG ATC AAG AAC ATC AGC GAC GCC CTG GGC AAG |     |     |  |     |  |     | 866  |
| Glu Lys Leu Asp Ala Gln Ile Lys Asn Ile Ser Asp Ala Leu Gly Lys |     |     |  |     |  |     |      |
|                                                                 | 685 |     |  | 690 |  | 695 |      |
| AAG CCC ATC CCC GAG AAC ATC ACC GTG TAC CGC TGG TGC GGC ATG CCC |     |     |  |     |  |     | 914  |
| Lys Pro Ile Pro Glu Asn Ile Thr Val Tyr Arg Trp Cys Gly Met Pro |     |     |  |     |  |     |      |
|                                                                 | 700 |     |  | 705 |  | 710 |      |
| GAG TTC GGC TAC CAG ATC AGC GAC CCC CTG CCC AGC CTG AAG GAC TTC |     |     |  |     |  |     | 962  |
| Glu Phe Gly Tyr Gln Ile Ser Asp Pro Leu Pro Ser Leu Lys Asp Phe |     |     |  |     |  |     |      |
|                                                                 | 715 |     |  | 720 |  | 725 |      |
| GAG GAG CAG TTC CTG AAC ACC ATC AAG GAG GAC AAG GGC TAC ATG AGC |     |     |  |     |  |     | 1010 |
| Glu Glu Gln Phe Leu Asn Thr Ile Lys Glu Asp Lys Gly Tyr Met Ser |     |     |  |     |  |     |      |
|                                                                 | 730 |     |  | 735 |  | 740 |      |
| ACC AGC CTG AGC AGC GAG CGC CTG GCC GCC TTC GGC AGC CGC AAG ATC |     |     |  |     |  |     | 1058 |
| Thr Ser Leu Ser Ser Glu Arg Leu Ala Ala Phe Gly Ser Arg Lys Ile |     |     |  |     |  |     |      |
|                                                                 | 745 |     |  | 750 |  | 755 | 760  |
| ATC CTG CGC CTG CAG GTG CCC AAG GGC AGC ACT GGT GCC TAC CTG AGC |     |     |  |     |  |     | 1106 |
| Ile Leu Arg Leu Gln Val Pro Lys Gly Ser Thr Gly Ala Tyr Leu Ser |     |     |  |     |  |     |      |
|                                                                 | 765 |     |  | 770 |  | 775 |      |
| GCC ATC GGC GGC TTC GCC AGC GAG AAG GAG ATC CTG CTG GAT AAG GAC |     |     |  |     |  |     | 1154 |
| Ala Ile Gly Gly Phe Ala Ser Glu Lys Glu Ile Leu Leu Asp Lys Asp |     |     |  |     |  |     |      |
|                                                                 | 780 |     |  | 785 |  | 790 |      |
| AGC AAG TAC CAC ATC GAC AAG GTG ACC GAG GTG ATC ATC AAG GGC GTG |     |     |  |     |  |     | 1202 |
| Ser Lys Tyr His Ile Asp Lys Val Thr Glu Val Ile Ile Lys Gly Val |     |     |  |     |  |     |      |
|                                                                 | 795 |     |  | 800 |  | 805 |      |
| AAG CGC TAC GTG GTG GAC GCC ACC CTG CTG ACC AAC TAG             |     |     |  |     |  |     | 1241 |

- 120 -

Lys Arg Tyr Val Val Asp Ala Thr Leu Leu Thr Asn  
 810 815 820

## (2) INFORMATION FOR SEQ ID NO:43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met Leu Gln Asn Leu Lys Ile Thr Asp Lys Val Glu Asp Phe Lys Glu  
 1 5 10 15  
 Asp Lys Glu Lys Ala Lys Glu Trp Gly Lys Glu Lys Glu Lys Glu Trp  
 20 25 30  
 Lys Leu Thr Ala Thr Glu Lys Gly Lys Met Asn Asn Phe Leu Asp Asn  
 35 40 45  
 Lys Asn Asp Ile Lys Thr Asn Tyr Lys Glu Ile Thr Phe Ser Ile Ala  
 50 55 60  
 Gly Ser Phe Glu Asp Glu Ile Lys Asp Leu Lys Glu Ile Asp Lys Met  
 65 70 75 80  
 Phe Asp Lys Thr Asn Leu Ser Asn Ser Ile Ile Thr Tyr Lys Asn Val  
 85 90 95  
 Glu Pro Thr Thr Ile Gly Phe Asn Lys Ser Leu Thr Glu Gly Asn Thr  
 100 105 110  
 Ile Asn Ser Asp Ala Met Ala Gln Phe Lys Glu Gln Phe Leu Asp Arg  
 115 120 125  
 Asp Ile Lys Phe Asp Ser Tyr Leu Asp Thr His Leu Thr Ala Gln Gln  
 130 135 140  
 Val Ser Ser Lys Glu Arg Val Ile Leu Lys Val Thr Val Pro Ser Gly  
 145 150 155 160  
 Lys Gly Ser Thr Thr Pro Thr Lys Ala Gly Val Ile Leu Asn Asn Ser  
 165 170 175  
 Glu Tyr Lys Met Leu Ile Asp Asn Gly Tyr Met Val His Val Asp Lys  
 180 185 190  
 Val Ser Lys Val Val Lys Lys Gly Val Glu Cys Leu Gln Ile Glu Gly  
 195 200 205  
 Thr Leu Lys Lys Ser Leu Asp Phe Lys Asn Asp Ile Asn Ala Glu Ala

- 121 -

|                                                                 |     |             |
|-----------------------------------------------------------------|-----|-------------|
| 210                                                             | 215 | 220         |
| His Ser Trp Gly Met Lys Asn Tyr Glu Glu Trp Ala Lys Asp Leu Thr |     |             |
| 225                                                             | 230 | 235 240     |
| Asp Ser Gln Arg Glu Ala Leu Asp Gly Tyr Ala Arg Gln Asp Tyr Lys |     |             |
|                                                                 | 245 | 250 255     |
| Glu Ile Asn Asn Tyr Leu Arg Asn Gln Gly Gly Ser Gly Asn Glu Lys |     |             |
|                                                                 | 260 | 265 270     |
| Leu Asp Ala Gln Ile Lys Asn Ile Ser Asp Ala Leu Gly Lys Lys Pro |     |             |
|                                                                 | 275 | 280 285     |
| Ile Pro Glu Asn Ile Thr Val Tyr Arg Trp Cys Gly Met Pro Glu Phe |     |             |
|                                                                 | 290 | 295 300     |
| Gly Tyr Gln Ile Ser Asp Pro Leu Pro Ser Leu Lys Asp Phe Glu Glu |     |             |
|                                                                 | 310 | 315 320     |
| Gln Phe Leu Asn Thr Ile Lys Glu Asp Lys Gly Tyr Met Ser Thr Ser |     |             |
|                                                                 | 325 | 330 335     |
| Leu Ser Ser Glu Arg Leu Ala Ala Phe Gly Ser Arg Lys Ile Ile Leu |     |             |
|                                                                 | 340 | 345 350     |
| Arg Leu Gln Val Pro Lys Gly Ser Thr Gly Ala Tyr Leu Ser Ala Ile |     |             |
|                                                                 | 355 | 360 365     |
| Gly Gly Phe Ala Ser Glu Lys Glu Ile Leu Leu Asp Lys Asp Ser Lys |     |             |
|                                                                 | 370 | 375 380     |
| Tyr His Ile Asp Lys Val Thr Glu Val Ile Ile Lys Gly Val Lys Arg |     |             |
|                                                                 | 385 | 390 395 400 |
| Tyr Val Val Asp Ala Thr Leu Leu Thr Asn                         |     |             |
|                                                                 | 405 | 410         |

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide encoding vacuolar targetting peptide used to construct pCIB5533"

## (iii) HYPOTHETICAL: NO

- 122 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

|                                                                  |    |
|------------------------------------------------------------------|----|
| CCGCGGGCGT GCACTGCCTC AGCAGCAGCA GCTTCGCGA CAGCAACCCC ATCCGCGTGA | 60 |
| CCGACCGCGC CGCCAGCACC CTGCAG                                     | 86 |

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 9..1355
- (D) OTHER INFORMATION: /note= "Maize optimized VIP2A(a) with the Bacillus secretion signal removed and the vacuolar targetting signal inserted as contained in pCIB5533"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| GATCCACC ATG GGC TGG AGC TGG ATC TTC CTG TTC CTG CTG AGC GGC GCC | 50  |
| Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala          |     |
| 415 420                                                          |     |
| GCG GGC GTG CAC TGC CTC AGC AGC AGC AGC TTC GCC GAC AGC AAC CCC  | 98  |
| Ala Gly Val His Cys Leu Ser Ser Ser Ser Phe Ala Asp Ser Asn Pro  |     |
| 425 430 435 440                                                  |     |
| ATC CGC GTG ACC GAC CGC GCC GCC AGC ACC CTG CAG AAC CTG AAG ATC  | 146 |
| Ile Arg Val Thr Asp Arg Ala Ala Ser Thr Leu Gln Asn Leu Lys Ile  |     |
| 445 450 455                                                      |     |
| ACC GAC AAG GTG GAG GAC TTC AAG GAG GAC AAG GAG AAG GCC AAG GAG  | 194 |
| Thr Asp Lys Val Glu Asp Phe Lys Glu Asp Lys Glu Lys Ala Lys Glu  |     |
| 460 465 470                                                      |     |
| TGG GGC AAG GAG AAG GAG AAG GAG TGG AAG CTT ACC GCC ACC GAG AAG  | 242 |
| Trp Gly Lys Glu Lys Glu Lys Glu Trp Lys Leu Thr Ala Thr Glu Lys  |     |
| 475 480 485                                                      |     |
| GGC AAG ATG AAC AAC TTC CTG GAC AAC AAG AAC GAC ATC AAG ACC AAC  | 290 |
| Gly Lys Met Asn Asn Phe Leu Asp Asn Lys Asn Asp Ile Lys Thr Asn  |     |
| 490 495 500                                                      |     |
| TAC AAG GAG ATC ACC TTC AGC ATA GCC GGC AGC TTC GAG GAC GAG ATC  | 338 |



- 123 -

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Lys | Glu | Ile | Thr | Phe | Ser | Ile | Ala | Gly | Ser | Phe | Glu | Asp | Glu | Ile |     |
| 505 |     |     |     |     | 510 |     |     |     |     | 515 |     |     |     |     | 520 |     |
| AAG | GAC | CTG | AAG | GAG | ATC | GAC | AAG | ATG | TTC | GAC | AAG | ACC | AAC | CTG | AGC | 386 |
| Lys | Asp | Leu | Lys | Glu | Ile | Asp | Lys | Met | Phe | Asp | Lys | Thr | Asn | Leu | Ser |     |
|     |     |     |     | 525 |     |     |     |     | 530 |     |     |     |     | 535 |     |     |
| AAC | AGC | ATC | ATC | ACC | TAC | AAG | AAC | GTG | GAG | CCC | ACC | ACC | ATC | GGC | TTC | 434 |
| Asn | Ser | Ile | Ile | Thr | Tyr | Lys | Asn | Val | Glu | Pro | Thr | Thr | Ile | Gly | Phe |     |
|     |     |     |     | 540 |     |     |     | 545 |     |     |     |     | 550 |     |     |     |
| AAC | AAG | AGC | CTG | ACC | GAG | GGC | AAC | ACC | ATC | AAC | AGC | GAC | GCC | ATG | GCC | 482 |
| Asn | Lys | Ser | Leu | Thr | Glu | Gly | Asn | Thr | Ile | Asn | Ser | Asp | Ala | Met | Ala |     |
|     |     | 555 |     |     |     |     | 560 |     |     |     |     | 565 |     |     |     |     |
| CAG | TTC | AAG | GAG | CAG | TTC | CTG | GAC | CGC | GAC | ATC | AAG | TTC | GAC | AGC | TAC | 530 |
| Gln | Phe | Lys | Glu | Gln | Phe | Leu | Asp | Arg | Asp | Ile | Lys | Phe | Asp | Ser | Tyr |     |
|     | 570 |     |     |     |     | 575 |     |     |     |     |     | 580 |     |     |     |     |
| CTG | GAC | ACC | CAC | CTG | ACC | GCC | CAG | CAG | GTG | AGC | AGC | AAG | GAG | CGC | GTG | 578 |
| Leu | Asp | Thr | His | Leu | Thr | Ala | Gln | Gln | Val | Ser | Ser | Lys | Glu | Arg | Val |     |
| 585 |     |     |     |     | 590 |     |     |     |     | 595 |     |     |     |     | 600 |     |
| ATC | CTG | AAG | GTG | ACC | GTC | CCC | AGC | GGC | AAG | GGC | AGC | ACC | ACC | CCC | ACC | 626 |
| Ile | Leu | Lys | Val | Thr | Val | Pro | Ser | Gly | Lys | Gly | Ser | Thr | Thr | Pro | Thr |     |
|     |     |     |     | 605 |     |     |     |     | 610 |     |     |     |     | 615 |     |     |
| AAG | GCC | GGC | GTG | ATC | CTG | AAC | AAC | AGC | GAG | TAC | AAG | ATG | CTG | ATC | GAC | 674 |
| Lys | Ala | Gly | Val | Ile | Leu | Asn | Asn | Ser | Glu | Tyr | Lys | Met | Leu | Ile | Asp |     |
|     |     |     | 620 |     |     |     |     | 625 |     |     |     | 630 |     |     |     |     |
| AAC | GGC | TAC | ATG | GTG | CAC | GTG | GAC | AAG | GTG | AGC | AAG | GTG | GTG | AAG | AAG | 722 |
| Asn | Gly | Tyr | Met | Val | His | Val | Asp | Lys | Val | Ser | Lys | Val | Val | Lys | Lys |     |
|     |     | 635 |     |     |     |     | 640 |     |     |     |     | 645 |     |     |     |     |
| GGC | GTG | GAG | TGC | CTC | CAG | ATC | GAG | GGC | ACC | CTG | AAG | AAG | AGT | CTA | GAC | 770 |
| Gly | Val | Glu | Cys | Leu | Gln | Ile | Glu | Gly | Thr | Leu | Lys | Lys | Ser | Leu | Asp |     |
|     | 650 |     |     |     |     | 655 |     |     |     |     |     | 660 |     |     |     |     |
| TTC | AAG | AAC | GAC | ATC | AAC | GCC | GAG | GCC | CAC | AGC | TGG | GGC | ATG | AAG | AAC | 818 |
| Phe | Lys | Asn | Asp | Ile | Asn | Ala | Glu | Ala | His | Ser | Trp | Gly | Met | Lys | Asn |     |
| 665 |     |     |     |     | 670 |     |     |     |     | 675 |     |     |     |     | 680 |     |
| TAC | GAG | GAG | TGG | GCC | AAG | GAC | CTG | ACC | GAC | AGC | CAG | CGC | GAG | GCC | CTG | 866 |
| Tyr | Glu | Glu | Trp | Ala | Lys | Asp | Leu | Thr | Asp | Ser | Gln | Arg | Glu | Ala | Leu |     |
|     |     |     |     | 685 |     |     |     |     | 690 |     |     |     |     | 695 |     |     |
| GAC | GGC | TAC | GCC | CGC | CAG | GAC | TAC | AAG | GAG | ATC | AAC | AAC | TAC | CTG | CGC | 914 |
| Asp | Gly | Tyr | Ala | Arg | Gln | Asp | Tyr | Lys | Glu | Ile | Asn | Asn | Tyr | Leu | Arg |     |
|     |     |     | 700 |     |     |     |     | 705 |     |     |     |     | 710 |     |     |     |
| AAC | CAG | GGC | GGC | AGC | GGC | AAC | GAG | AAG | CTG | GAC | GCC | CAG | ATC | AAG | AAC | 962 |
| Asn | Gln | Gly | Gly | Ser | Gly | Asn | Glu | Lys | Leu | Asp | Ala | Gln | Ile | Lys | Asn |     |
|     |     | 715 |     |     |     |     | 720 |     |     |     |     | 725 |     |     |     |     |

- 124 -

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| ATC AGC GAC GCC CTG GGC AAG AAG CCC ATC CCC GAG AAC ATC ACC GTG<br>Ile Ser Asp Ala Leu Gly Lys Lys Pro Ile Pro Glu Asn Ile Thr Val<br>730 735 740     | 1010 |
| TAC CGC TGG TGC GGC ATG CCC GAG TTC GGC TAC CAG ATC AGC GAC CCC<br>Tyr Arg Trp Cys Gly Met Pro Glu Phe Gly Tyr Gln Ile Ser Asp Pro<br>745 750 755 760 | 1058 |
| CTG CCC AGC CTG AAG GAC TTC GAG GAG CAG TTC CTG AAC ACC ATC AAG<br>Leu Pro Ser Leu Lys Asp Phe Glu Glu Gln Phe Leu Asn Thr Ile Lys<br>765 770 775     | 1106 |
| GAG GAC AAG GGC TAC ATG AGC ACC AGC CTG AGC AGC GAG CGC CTG GCC<br>Glu Asp Lys Gly Tyr Met Ser Thr Ser Leu Ser Ser Glu Arg Leu Ala<br>780 785 790     | 1154 |
| GCC TTC GGC AGC CGC AAG ATC ATC CTG CGC CTG CAG GTG CCC AAG GGC<br>Ala Phe Gly Ser Arg Lys Ile Ile Leu Arg Leu Gln Val Pro Lys Gly<br>795 800 805     | 1202 |
| AGC ACT GGT GCC TAC CTG AGC GCC ATC GGC GGC TTC GCC AGC GAG AAG<br>Ser Thr Gly Ala Tyr Leu Ser Ala Ile Gly Gly Phe Ala Ser Glu Lys<br>810 815 820     | 1250 |
| GAG ATC CTG CTG GAT AAG GAC AGC AAG TAC CAC ATC GAC AAG GTG ACC<br>Glu Ile Leu Leu Asp Lys Asp Ser Lys Tyr His Ile Asp Lys Val Thr<br>825 830 835 840 | 1298 |
| GAG GTG ATC ATC AAG GGC GTG AAG CGC TAC GTG GTG GAC GCC ACC CTG<br>Glu Val Ile Ile Lys Gly Val Lys Arg Tyr Val Val Asp Ala Thr Leu<br>845 850 855     | 1346 |
| CTG ACC AAC TAG<br>Leu Thr Asn                                                                                                                        | 1358 |

## (2) INFORMATION FOR SEQ ID NO:46:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 449 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

|                                                                              |
|------------------------------------------------------------------------------|
| Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly<br>1 5 10 15 |
| Val His Cys Leu Ser Ser Ser Ser Phe Ala Asp Ser Asn Pro Ile Arg<br>20 25 30  |
| Val Thr Asp Arg Ala Ala Ser Thr Leu Gln Asn Leu Lys Ile Thr Asp              |

- 125 -

| 35                                                              | 40  | 45      |
|-----------------------------------------------------------------|-----|---------|
| Lys Val Glu Asp Phe Lys Glu Asp Lys Glu Lys Ala Lys Glu Trp Gly |     |         |
| 50                                                              | 55  | 60      |
| Lys Glu Lys Glu Lys Glu Trp Lys Leu Thr Ala Thr Glu Lys Gly Lys |     |         |
| 65                                                              | 70  | 75 80   |
| Met Asn Asn Phe Leu Asp Asn Lys Asn Asp Ile Lys Thr Asn Tyr Lys |     |         |
|                                                                 | 85  | 90 95   |
| Glu Ile Thr Phe Ser Ile Ala Gly Ser Phe Glu Asp Glu Ile Lys Asp |     |         |
| 100                                                             | 105 | 110     |
| Leu Lys Glu Ile Asp Lys Met Phe Asp Lys Thr Asn Leu Ser Asn Ser |     |         |
| 115                                                             | 120 | 125     |
| Ile Ile Thr Tyr Lys Asn Val Glu Pro Thr Thr Ile Gly Phe Asn Lys |     |         |
| 130                                                             | 135 | 140     |
| Ser Leu Thr Glu Gly Asn Thr Ile Asn Ser Asp Ala Met Ala Gln Phe |     |         |
| 145                                                             | 150 | 155 160 |
| Lys Glu Gln Phe Leu Asp Arg Asp Ile Lys Phe Asp Ser Tyr Leu Asp |     |         |
|                                                                 | 165 | 170 175 |
| Thr His Leu Thr Ala Gln Gln Val Ser Ser Lys Glu Arg Val Ile Leu |     |         |
|                                                                 | 180 | 185 190 |
| Lys Val Thr Val Pro Ser Gly Lys Gly Ser Thr Thr Pro Thr Lys Ala |     |         |
| 195                                                             | 200 | 205     |
| Gly Val Ile Leu Asn Asn Ser Glu Tyr Lys Met Leu Ile Asp Asn Gly |     |         |
| 210                                                             | 215 | 220     |
| Tyr Met Val His Val Asp Lys Val Ser Lys Val Val Lys Lys Gly Val |     |         |
| 225                                                             | 230 | 235 240 |
| Glu Cys Leu Gln Ile Glu Gly Thr Leu Lys Lys Ser Leu Asp Phe Lys |     |         |
|                                                                 | 245 | 250 255 |
| Asn Asp Ile Asn Ala Glu Ala His Ser Trp Gly Met Lys Asn Tyr Glu |     |         |
|                                                                 | 260 | 265 270 |
| Glu Trp Ala Lys Asp Leu Thr Asp Ser Gln Arg Glu Ala Leu Asp Gly |     |         |
| 275                                                             | 280 | 285     |
| Tyr Ala Arg Gln Asp Tyr Lys Glu Ile Asn Asn Tyr Leu Arg Asn Gln |     |         |
| 290                                                             | 295 | 300     |
| Gly Gly Ser Gly Asn Glu Lys Leu Asp Ala Gln Ile Lys Asn Ile Ser |     |         |
| 305                                                             | 310 | 315 320 |
| Asp Ala Leu Gly Lys Lys Pro Ile Pro Glu Asn Ile Thr Val Tyr Arg |     |         |
|                                                                 | 325 | 330 335 |

- 126 -

Trp Cys Gly Met Pro Glu Phe Gly Tyr Gln Ile Ser Asp Pro Leu Pro  
 340 345 350

Ser Leu Lys Asp Phe Glu Glu Gln Phe Leu Asn Thr Ile Lys Glu Asp  
 355 360 365

Lys Gly Tyr Met Ser Thr Ser Leu Ser Ser Glu Arg Leu Ala Ala Phe  
 370 375 380

Gly Ser Arg Lys Ile Ile Leu Arg Leu Gln Val Pro Lys Gly Ser Thr  
 385 390 395 400

Gly Ala Tyr Leu Ser Ala Ile Gly Gly Phe Ala Ser Glu Lys Glu Ile  
 405 410 415

Leu Leu Asp Lys Asp Ser Lys Tyr His Ile Asp Lys Val Thr Glu Val  
 420 425 430

Ile Ile Lys Gly Val Lys Arg Tyr Val Val Asp Ala Thr Leu Leu Thr  
 435 440 445

Asn

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "linker peptide for fusion of VIP1A(a) and VIP2A(a) used to construct pCIB5533"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid

- 127 -

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA encoding linker peptide  
used to construct pCIB5533"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

|                                                                 |    |
|-----------------------------------------------------------------|----|
| CCCCGGCCTT CTACTCCCC AACTCCCTCT CCTAGCAGC CTCCGACACC TAGCGATATC | 60 |
| GGATCC                                                          | 66 |

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4031 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 6..4019

(D) OTHER INFORMATION: /note= "Maize optimized DNA  
sequence encoding a VIP2A(a) - VIP1A(a) fusion protein as  
contained in pCIB5531"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GATCC ATG AAG CGC ATG GAG GGC AAG CTG TTC ATG GTG AGC AAG AAG   | 47  |
| Met Lys Arg Met Glu Gly Lys Leu Phe Met Val Ser Lys Lys         |     |
| 450 455 460                                                     |     |
| CTC CAG GTG GTG ACC AAG ACC GTG CTG CTG AGC ACC GTG TTC AGC ATC | 95  |
| Leu Gln Val Val Thr Lys Thr Val Leu Leu Ser Thr Val Phe Ser Ile |     |
| 465 470 475                                                     |     |
| AGC CTG CTG AAC AAC GAG GTG ATC AAG GCC GAG CAG CTG AAC ATC AAC | 143 |
| Ser Leu Leu Asn Asn Glu Val Ile Lys Ala Glu Gln Leu Asn Ile Asn |     |
| 480 485 490 495                                                 |     |
| AGC CAG AGC AAG TAC ACC AAC CTC CAG AAC CTG AAG ATC ACC GAC AAG | 191 |

- 128 -

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gln | Ser | Lys | Tyr | Thr | Asn | Leu | Gln | Asn | Leu | Lys | Ile | Thr | Asp | Lys |     |
|     |     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| GTG | GAG | GAC | TTC | AAG | GAG | GAC | AAG | GAG | AAG | GCC | AAG | GAG | TGG | GGC | AAG | 239 |
| Val | Glu | Asp | Phe | Lys | Glu | Asp | Lys | Glu | Lys | Ala | Lys | Glu | Trp | Gly | Lys |     |
|     |     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| GAG | AAG | GAG | AAG | GAG | TGG | AAG | CTT | ACC | GCC | ACC | GAG | AAG | GGC | AAG | ATG | 287 |
| Glu | Lys | Glu | Lys | Glu | Trp | Lys | Leu | Thr | Ala | Thr | Glu | Lys | Gly | Lys | Met |     |
|     |     |     | 530 |     |     |     | 535 |     |     |     |     |     | 540 |     |     |     |
| AAC | AAC | TTC | CTG | GAC | AAC | AAG | AAC | GAC | ATC | AAG | ACC | AAC | TAC | AAG | GAG | 335 |
| Asn | Asn | Phe | Leu | Asp | Asn | Lys | Asn | Asp | Ile | Lys | Thr | Asn | Tyr | Lys | Glu |     |
|     |     |     | 545 |     |     | 550 |     |     |     |     | 555 |     |     |     |     |     |
| ATC | ACC | TTC | AGC | ATA | GCC | GGC | AGC | TTC | GAG | GAC | GAG | ATC | AAG | GAC | CTG | 383 |
| Ile | Thr | Phe | Ser | Ile | Ala | Gly | Ser | Phe | Glu | Asp | Glu | Ile | Lys | Asp | Leu |     |
| 560 |     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |
| AAG | GAG | ATC | GAC | AAG | ATG | TTC | GAC | AAG | ACC | AAC | CTG | AGC | AAC | AGC | ATC | 431 |
| Lys | Glu | Ile | Asp | Lys | Met | Phe | Asp | Lys | Thr | Asn | Leu | Ser | Asn | Ser | Ile |     |
|     |     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |
| ATC | ACC | TAC | AAG | AAC | GTG | GAG | CCC | ACC | ACC | ATC | GGC | TTC | AAC | AAG | AGC | 479 |
| Ile | Thr | Tyr | Lys | Asn | Val | Glu | Pro | Thr | Thr | Ile | Gly | Phe | Asn | Lys | Ser |     |
|     |     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |
| CTG | ACC | GAG | GGC | AAC | ACC | ATC | AAC | AGC | GAC | GCC | ATG | GCC | CAG | TTC | AAG | 527 |
| Leu | Thr | Glu | Gly | Asn | Thr | Ile | Asn | Ser | Asp | Ala | Met | Ala | Gln | Phe | Lys |     |
|     |     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |
| GAG | CAG | TTC | CTG | GAC | CGC | GAC | ATC | AAG | TTC | GAC | AGC | TAC | CTG | GAC | ACC | 575 |
| Glu | Gln | Phe | Leu | Asp | Arg | Asp | Ile | Lys | Phe | Asp | Ser | Tyr | Leu | Asp | Thr |     |
|     |     | 625 |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     |     |
| CAC | CTG | ACC | GCC | CAG | CAG | GTG | AGC | AGC | AAG | GAG | CGC | GTG | ATC | CTG | AAG | 623 |
| His | Leu | Thr | Ala | Gln | Gln | Val | Ser | Ser | Lys | Glu | Arg | Val | Ile | Leu | Lys |     |
| 640 |     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |
| GTG | ACC | GTC | CCC | AGC | GGC | AAG | GGC | AGC | ACC | ACC | CCC | ACC | AAG | GCC | GGC | 671 |
| Val | Thr | Val | Pro | Ser | Gly | Lys | Gly | Ser | Thr | Thr | Pro | Thr | Lys | Ala | Gly |     |
|     |     |     |     | 660 |     |     |     |     | 665 |     |     |     |     | 670 |     |     |
| GTG | ATC | CTG | AAC | AAC | AGC | GAG | TAC | AAG | ATG | CTG | ATC | GAC | AAC | GGC | TAC | 719 |
| Val | Ile | Leu | Asn | Asn | Ser | Glu | Tyr | Lys | Met | Leu | Ile | Asp | Asn | Gly | Tyr |     |
|     |     |     | 675 |     |     |     |     | 680 |     |     |     |     |     | 685 |     |     |
| ATG | GTG | CAC | GTG | GAC | AAG | GTG | AGC | AAG | GTG | GTG | AAG | AAG | GGC | GTG | GAG | 767 |
| Met | Val | His | Val | Asp | Lys | Val | Ser | Lys | Val | Val | Lys | Lys | Gly | Val | Glu |     |
|     |     |     | 690 |     |     |     |     | 695 |     |     |     |     | 700 |     |     |     |
| TGC | CTC | CAG | ATC | GAG | GGC | ACC | CTG | AAG | AAG | AGT | CTA | GAC | TTC | AAG | AAC | 815 |
| Cys | Leu | Gln | Ile | Glu | Gly | Thr | Leu | Lys | Lys | Ser | Leu | Asp | Phe | Lys | Asn |     |
|     |     | 705 |     |     |     |     | 710 |     |     |     |     | 715 |     |     |     |     |

- 129 -

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| GAC ATC AAC GCC GAG GCC CAC AGC TGG GGC ATG AAG AAC TAC GAG GAG<br>Asp Ile Asn Ala Glu Ala His Ser Trp Gly Met Lys Asn Tyr Glu Glu<br>720 725 730 735 | 863  |
| TGG GCC AAG GAC CTG ACC GAC AGC CAG CGC GAG GCC CTG GAC GGC TAC<br>Trp Ala Lys Asp Leu Thr Asp Ser Gln Arg Glu Ala Leu Asp Gly Tyr<br>740 745 750     | 911  |
| GCC CGC CAG GAC TAC AAG GAG ATC AAC AAC TAC CTG CGC AAC CAG GGC<br>Ala Arg Gln Asp Tyr Lys Glu Ile Asn Asn Tyr Leu Arg Asn Gln Gly<br>755 760 765     | 959  |
| GGC AGC GGC AAC GAG AAG CTG GAC GCC CAG ATC AAG AAC ATC AGC GAC<br>Gly Ser Gly Asn Glu Lys Leu Asp Ala Gln Ile Lys Asn Ile Ser Asp<br>770 775 780     | 1007 |
| GCC CTG GGC AAG AAG CCC ATC CCC GAG AAC ATC ACC GTG TAC CGC TGG<br>Ala Leu Gly Lys Lys Pro Ile Pro Glu Asn Ile Thr Val Tyr Arg Trp<br>785 790 795     | 1055 |
| TGC GGC ATG CCC GAG TTC GGC TAC CAG ATC AGC GAC CCC CTG CCC AGC<br>Cys Gly Met Pro Glu Phe Gly Tyr Gln Ile Ser Asp Pro Leu Pro Ser<br>800 805 810 815 | 1103 |
| CTG AAG GAC TTC GAG GAG CAG TTC CTG AAC ACC ATC AAG GAG GAC AAG<br>Leu Lys Asp Phe Glu Glu Gln Phe Leu Asn Thr Ile Lys Glu Asp Lys<br>820 825 830     | 1151 |
| GGC TAC ATG AGC ACC AGC CTG AGC AGC GAG CGC CTG GCC GCC TTC GGC<br>Gly Tyr Met Ser Thr Ser Leu Ser Ser Glu Arg Leu Ala Ala Phe Gly<br>835 840 845     | 1199 |
| AGC CGC AAG ATC ATC CTG CGC CTG CAG GTG CCC AAG GGC AGC ACT GGT<br>Ser Arg Lys Ile Ile Leu Arg Leu Gln Val Pro Lys Gly Ser Thr Gly<br>850 855 860     | 1247 |
| GCC TAC CTG AGC GCC ATC GGC GGC TTC GCC AGC GAG AAG GAG ATC CTG<br>Ala Tyr Leu Ser Ala Ile Gly Gly Phe Ala Ser Glu Lys Glu Ile Leu<br>865 870 875     | 1295 |
| CTG GAT AAG GAC AGC AAG TAC CAC ATC GAC AAG GTG ACC GAG GTG ATC<br>Leu Asp Lys Asp Ser Lys Tyr His Ile Asp Lys Val Thr Glu Val Ile<br>880 885 890 895 | 1343 |
| ATC AAG GGC GTG AAG CGC TAC GTG GTG GAC GCC ACC CTG CTG ACC AAC<br>Ile Lys Gly Val Lys Arg Tyr Val Val Asp Ala Thr Leu Leu Thr Asn<br>900 905 910     | 1391 |
| TCC CGG GGG CCT TCT ACT CCC CCA ACT CCC TCT CCT AGC ACG CCT CCG<br>Ser Arg Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro<br>915 920 925     | 1439 |
| ACA CCT AGC GAT ATC GGA TCC ACC ATG AAG ACC AAC CAG ATC AGC ACC<br>Thr Pro Ser Asp Ile Gly Ser Thr Met Lys Thr Asn Gln Ile Ser Thr<br>930 935 940     | 1487 |

- 130 -

|                                                                                                                                                           |      |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| ACC CAG AAG AAC CAG CAG AAG GAG ATG GAC CGC AAG GGC CTG CTG GGC<br>Thr Gln Lys Asn Gln Gln Lys Glu Met Asp Arg Lys Gly Leu Leu Gly<br>945 950 955         | 1535 |
| TAC TAC TTC AAG GGC AAG GAC TTC AGC AAC CTG ACC ATG TTC GCC CCC<br>Tyr Tyr Phe Lys Gly Lys Asp Phe Ser Asn Leu Thr Met Phe Ala Pro<br>960 965 970 975     | 1583 |
| ACG CGT GAC AGC ACC CTG ATC TAC GAC CAG CAG ACC GCC AAC AAG CTG<br>Thr Arg Asp Ser Thr Leu Ile Tyr Asp Gln Gln Thr Ala Asn Lys Leu<br>980 985 990         | 1631 |
| CTG GAC AAG AAG CAG CAG GAG TAC CAG AGC ATC CGC TGG ATC GGC CTG<br>Leu Asp Lys Lys Gln Gln Glu Tyr Gln Ser Ile Arg Trp Ile Gly Leu<br>995 1000 1005       | 1679 |
| ATC CAG AGC AAG GAG ACC GGC GAC TTC ACC TTC AAC CTG AGC GAG GAC<br>Ile Gln Ser Lys Glu Thr Gly Asp Phe Thr Phe Asn Leu Ser Glu Asp<br>1010 1015 1020      | 1727 |
| GAG CAG GCC ATC ATC GAG ATC AAC GGC AAG ATC ATC AGC AAC AAG GGC<br>Glu Gln Ala Ile Ile Glu Ile Asn Gly Lys Ile Ile Ser Asn Lys Gly<br>1025 1030 1035      | 1775 |
| AAG GAG AAG CAG GTG GTG CAC CTG GAG AAG GGC AAG CTG GTG CCC ATC<br>Lys Glu Lys Lys Val Val His Leu Glu Lys Gly Lys Leu Val Pro Ile<br>1040 1045 1050 1055 | 1823 |
| AAG ATC GAG TAC CAG AGC GAC ACC AAG TTC AAC ATC GAC AGC AAG ACC<br>Lys Ile Glu Tyr Gln Ser Asp Thr Lys Phe Asn Ile Asp Ser Lys Thr<br>1060 1065 1070      | 1871 |
| TTC AAG GAG CTG AAG CTT TTC AAG ATC GAC AGC CAG AAC CAG CCC CAG<br>Phe Lys Glu Leu Lys Leu Phe Lys Ile Asp Ser Gln Asn Gln Pro Gln<br>1075 1080 1085      | 1919 |
| CAG GTG CAG CAG GAC GAG CTG CGC AAC CCC GAG TTC AAC AAG AAG GAG<br>Gln Val Gln Gln Asp Glu Leu Arg Asn Pro Glu Phe Asn Lys Lys Glu<br>1090 1095 1100      | 1967 |
| AGC CAG GAG TTC CTG GCC AAG CCC AGC AAG ATC AAC CTG TTC ACC CAG<br>Ser Gln Glu Phe Leu Ala Lys Pro Ser Lys Ile Asn Leu Phe Thr Gln<br>1105 1110 1115      | 2015 |
| CAG ATG AAG CGC GAG ATC GAC GAG GAC ACC GAC ACC GAC GGC GAC AGC<br>Gln Met Lys Arg Glu Ile Asp Glu Asp Thr Asp Thr Asp Gly Asp Ser<br>1120 1125 1130 1135 | 2063 |
| ATC CCC GAC CTG TGG GAG GAG AAC GGC TAC ACC ATC CAG AAC CGC ATC<br>Ile Pro Asp Leu Trp Glu Glu Asn Gly Tyr Thr Ile Gln Asn Arg Ile<br>1140 1145 1150      | 2111 |
| GCC GTG AAG TGG GAC GAC AGC CTG GCT AGC AAG GGC TAC ACC AAG TTC<br>Ala Val Lys Trp Asp Asp Ser Leu Ala Ser Lys Gly Tyr Thr Lys Phe<br>2159                |      |



- 131 -

| 1155                                                                                                                                                      | 1160 | 1165 |      |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------|------|------|------|
| GTG AGC AAC CCC CTG GAG AGC CAC ACC GTG GGC GAC CCC TAC ACC GAC<br>Val Ser Asn Pro Leu Glu Ser His Thr Val Gly Asp Pro Tyr Thr Asp<br>1170 1175 1180      |      |      | 2207 |
| TAC GAG AAG GCC GCC CGC GAC CTG GAC CTG AGC AAC GCC AAG GAG ACC<br>Tyr Glu Lys Ala Ala Arg Asp Leu Asp Leu Ser Asn Ala Lys Glu Thr<br>1185 1190 1195      |      |      | 2255 |
| TTC AAC CCC CTG GTG GCC GCC TTC CCC AGC GTG AAC GTG AGC ATG GAG<br>Phe Asn Pro Leu Val Ala Ala Phe Pro Ser Val Asn Val Ser Met Glu<br>1200 1205 1210 1215 |      |      | 2303 |
| AAG GTG ATC CTG AGC CCC AAC GAG AAC CTG AGC AAC AGC GTG GAG AGC<br>Lys Val Ile Leu Ser Pro Asn Glu Asn Leu Ser Asn Ser Val Glu Ser<br>1220 1225 1230      |      |      | 2351 |
| CAC TCG AGC ACC AAC TGG AGC TAC ACC AAC ACC GAG GGC GCC AGC GTG<br>His Ser Ser Thr Asn Trp Ser Tyr Thr Asn Thr Glu Gly Ala Ser Val<br>1235 1240 1245      |      |      | 2399 |
| GAG GCC GGC ATC GGT CCC AAG GGC ATC AGC TTC GGC GTG AGC GTG AAC<br>Glu Ala Gly Ile Gly Pro Lys Gly Ile Ser Phe Gly Val Ser Val Asn<br>1250 1255 1260      |      |      | 2447 |
| TAC CAG CAC AGC GAG ACC GTG GCC CAG GAG TGG GGC ACC AGC ACC GGC<br>Tyr Gln His Ser Glu Thr Val Ala Gln Glu Trp Gly Thr Ser Thr Gly<br>1265 1270 1275      |      |      | 2495 |
| AAC ACC AGC CAG TTC AAC ACC GCC AGC GCC GGC TAC CTG AAC GCC AAC<br>Asn Thr Ser Gln Phe Asn Thr Ala Ser Ala Gly Tyr Leu Asn Ala Asn<br>1280 1285 1290 1295 |      |      | 2543 |
| GTG CGC TAC AAC AAC GTG GGC ACC GGC GCC ATC TAC GAC GTG AAG CCC<br>Val Arg Tyr Asn Asn Val Gly Thr Gly Ala Ile Tyr Asp Val Lys Pro<br>1300 1305 1310      |      |      | 2591 |
| ACC ACC AGC TTC GTG CTG AAC AAC GAC ACC ATC GCC ACC ATC ACC GCC<br>Thr Thr Ser Phe Val Leu Asn Asn Asp Thr Ile Ala Thr Ile Thr Ala<br>1315 1320 1325      |      |      | 2639 |
| AAG TCG AAT TCC ACC GCC CTG AAC ATC AGC CCC GGC GAG AGC TAC CCC<br>Lys Ser Asn Ser Thr Ala Leu Asn Ile Ser Pro Gly Glu Ser Tyr Pro<br>1330 1335 1340      |      |      | 2687 |
| AAG AAG GGC CAG AAC GGC ATC GCC ATC ACC AGC ATG GAC GAC TTC AAC<br>Lys Lys Gly Gln Asn Gly Ile Ala Ile Thr Ser Met Asp Asp Phe Asn<br>1345 1350 1355      |      |      | 2735 |
| AGC CAC CCC ATC ACC CTG AAC AAG AAG CAG GTG GAC AAC CTG CTG AAC<br>Ser His Pro Ile Thr Leu Asn Lys Lys Gln Val Asp Asn Leu Leu Asn<br>1360 1365 1370 1375 |      |      | 2783 |
| AAC AAG CCC ATG ATG CTG GAG ACC AAC CAG ACC GAC GGC GTC TAC AAG                                                                                           |      |      | 2831 |

- 132 -

|                                                                 |      |
|-----------------------------------------------------------------|------|
| Asn Lys Pro Met Met Leu Glu Thr Asn Gln Thr Asp Gly Val Tyr Lys |      |
| 1380 1385 1390                                                  |      |
| ATC AAG GAC ACC CAC GGC AAC ATC GTG ACG GGC GGC GAG TGG AAC GGC | 2879 |
| Ile Lys Asp Thr His Gly Asn Ile Val Thr Gly Gly Glu Trp Asn Gly |      |
| 1395 1400 1405                                                  |      |
| GTG ATC CAG CAG ATC AAG GCC AAG ACC GCC AGC ATC ATC GTC GAC GAC | 2927 |
| Val Ile Gln Gln Ile Lys Ala Lys Thr Ala Ser Ile Ile Val Asp Asp |      |
| 1410 1415 1420                                                  |      |
| GGC GAG CGC GTG GCC GAG AAG CGC GTG GCC GCC AAG GAC TAC GAG AAC | 2975 |
| Gly Glu Arg Val Ala Glu Lys Arg Val Ala Ala Lys Asp Tyr Glu Asn |      |
| 1425 1430 1435                                                  |      |
| CCC GAG GAC AAG ACC CCC AGC CTG ACC CTG AAG GAC GCC CTG AAG CTG | 3023 |
| Pro Glu Asp Lys Thr Pro Ser Leu Thr Leu Lys Asp Ala Leu Lys Leu |      |
| 1440 1445 1450 1455                                             |      |
| AGC TAC CCC GAC GAG ATC AAG GAG ATC GAG GGC TTG CTG TAC TAC AAG | 3071 |
| Ser Tyr Pro Asp Glu Ile Lys Glu Ile Glu Gly Leu Leu Tyr Tyr Lys |      |
| 1460 1465 1470                                                  |      |
| AAC AAG CCC ATC TAC GAG AGC AGC GTG ATG ACC TAT CTA GAC GAG AAC | 3119 |
| Asn Lys Pro Ile Tyr Glu Ser Ser Val Met Thr Tyr Leu Asp Glu Asn |      |
| 1475 1480 1485                                                  |      |
| ACC GCC AAG GAG GTG ACC AAG CAG CTG AAC GAC ACC ACC GGC AAG TTC | 3167 |
| Thr Ala Lys Glu Val Thr Lys Gln Leu Asn Asp Thr Thr Gly Lys Phe |      |
| 1490 1495 1500                                                  |      |
| AAG GAC GTG AGC CAC CTG TAC GAC GTG AAG CTG ACC CCC AAG ATG AAC | 3215 |
| Lys Asp Val Ser His Leu Tyr Asp Val Lys Leu Thr Pro Lys Met Asn |      |
| 1505 1510 1515                                                  |      |
| GTG ACC ATC AAG CTG AGC ATC CTG TAC GAC AAC GCC GAG AGC AAC GAC | 3263 |
| Val Thr Ile Lys Leu Ser Ile Leu Tyr Asp Asn Ala Glu Ser Asn Asp |      |
| 1520 1525 1530 1535                                             |      |
| AAC AGC ATC GGC AAG TGG ACC AAC ACC AAC ATC GTG AGC GGC GGC AAC | 3311 |
| Asn Ser Ile Gly Lys Trp Thr Asn Thr Asn Ile Val Ser Gly Gly Asn |      |
| 1540 1545 1550                                                  |      |
| AAC GGC AAG AAG CAG TAC AGC AGC AAC AAC CCC GAC GCC AAC CTG ACC | 3359 |
| Asn Gly Lys Lys Gln Tyr Ser Ser Asn Asn Pro Asp Ala Asn Leu Thr |      |
| 1555 1560 1565                                                  |      |
| CTG AAC ACC GAC GCC CAG GAG AAG CTG AAC AAG AAC CGC GAC TAC TAC | 3407 |
| Leu Asn Thr Asp Ala Gln Glu Lys Leu Asn Lys Asn Arg Asp Tyr Tyr |      |
| 1570 1575 1580                                                  |      |
| ATC AGC CTG TAC ATG AAG AGC GAG AAG AAC ACC CAG TGC GAG ATC ACC | 3455 |
| Ile Ser Leu Tyr Met Lys Ser Glu Lys Asn Thr Gln Cys Glu Ile Thr |      |
| 1585 1590 1595                                                  |      |

- 133 -

|                                                                                                                                                           |      |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| ATC GAC GGC GAG ATA TAC CCC ATC ACC ACC AAG ACC GTG AAC GTG AAC<br>Ile Asp Gly Glu Ile Tyr Pro Ile Thr Thr Lys Thr Val Asn Val Asn<br>1600 1605 1610 1615 | 3503 |
| AAG GAC AAC TAC AAG CGC CTG GAC ATC ATC GCC CAC AAC ATC AAG AGC<br>Lys Asp Asn Tyr Lys Arg Leu Asp Ile Ile Ala His Asn Ile Lys Ser<br>1620 1625 1630      | 3551 |
| AAC CCC ATC AGC AGC CTG CAC ATC AAG ACC AAC GAC GAG ATC ACC CTG<br>Asn Pro Ile Ser Ser Leu His Ile Lys Thr Asn Asp Glu Ile Thr Leu<br>1635 1640 1645      | 3599 |
| TTC-TGG GAC GAC ATA TCG ATT ACC GAC GTC GCC AGC ATC AAG CCC GAG<br>Phe Trp Asp Asp Ile Ser Ile Thr Asp Val Ala Ser Ile Lys Pro Glu<br>1650 1655 1660      | 3647 |
| AAC CTG ACC GAC AGC GAG ATC AAG CAG ATA TAC AGT CGC TAC GGC ATC<br>Asn Leu Thr Asp Ser Glu Ile Lys Gln Ile Tyr Ser Arg Tyr Gly Ile<br>1665 1670 1675      | 3695 |
| AAG CTG GAG GAC GGC ATC CTG ATC GAC AAG AAA GGC GGC ATC CAC TAC<br>Lys Leu Glu Asp Gly Ile Leu Ile Asp Lys Lys Gly Gly Ile His Tyr<br>1680 1685 1690 1695 | 3743 |
| GGC GAG TTC ATC AAC GAG GCC AGC TTC AAC ATC GAG CCC CTG CAG AAC<br>Gly Glu Phe Ile Asn Glu Ala Ser Phe Asn Ile Glu Pro Leu Gln Asn<br>1700 1705 1710      | 3791 |
| TAC GTG ACC AAG TAC GAG GTG ACC TAC AGC AGC GAG CTG GGC CCC AAC<br>Tyr Val Thr Lys Tyr Glu Val Thr Tyr Ser Ser Glu Leu Gly Pro Asn<br>1715 1720 1725      | 3839 |
| GTG AGC GAC ACC CTG GAG AGC GAC AAG ATT TAC AAG GAC GGC ACC ATC<br>Val Ser Asp Thr Leu Glu Ser Asp Lys Ile Tyr Lys Asp Gly Thr Ile<br>1730 1735 1740      | 3887 |
| AAG TTC GAC TTC ACC AAG TAC AGC AAG AAC GAG CAG GGC CTG TTC TAC<br>Lys Phe Asp Phe Thr Lys Tyr Ser Lys Asn Glu Gln Gly Leu Phe Tyr<br>1745 1750 1755      | 3935 |
| GAC AGC GGC CTG AAC TGG GAC TTC AAG ATC AAC GCC ATC ACC-TAC GAC<br>Asp Ser Gly Leu Asn Trp Asp Phe Lys Ile Asn Ala Ile Thr Tyr Asp<br>1760 1765 1770 1775 | 3983 |
| GGC AAG GAG ATG AAC GTG TTC CAC CGC TAC AAC AAG TAGATCTGAG<br>Gly Lys Glu Met Asn Val Phe His Arg Tyr Asn Lys<br>1780 1785                                | 4029 |
| CT                                                                                                                                                        | 4031 |

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1338 amino acids

- 134 -

(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```

Met Lys Arg Met Glu Gly Lys Leu Phe Met Val Ser Lys Lys Leu Gln
 1 5 10 15

Val Val Thr Lys Thr Val Leu Leu Ser Thr Val Phe Ser Ile Ser Leu
 20 25 30

Leu Asn Asn Glu Val Ile Lys Ala Glu Gln Leu Asn Ile Asn Ser Gln
 35 40 45

Ser Lys Tyr Thr Asn Leu Gln Asn Leu Lys Ile Thr Asp Lys Val Glu
 50 55 60

Asp Phe Lys Glu Asp Lys Glu Lys Ala Lys Glu Trp Gly Lys Glu Lys
 65 70 75 80

Glu Lys Glu Trp Lys Leu Thr Ala Thr Glu Lys Gly Lys Met Asn Asn
 85 90 95

Phe Leu Asp Asn Lys Asn Asp Ile Lys Thr Asn Tyr Lys Glu Ile Thr
 100 105 110

Phe Ser Ile Ala Gly Ser Phe Glu Asp Glu Ile Lys Asp Leu Lys Glu
 115 120 125

Ile Asp Lys Met Phe Asp Lys Thr Asn Leu Ser Asn Ser Ile Ile Thr
 130 135 140

Tyr Lys Asn Val Glu Pro Thr Thr Ile Gly Phe Asn Lys Ser Leu Thr
 145 150 155 160

Glu Gly Asn Thr Ile Asn Ser Asp Ala Met Ala Gln Phe Lys Glu Gln
 165 170 175

Phe Leu Asp Arg Asp Ile Lys Phe Asp Ser Tyr Leu Asp Thr His Leu
 180 185 190

Thr Ala Gln Gln Val Ser Ser Lys Glu Arg Val Ile Leu Lys Val Thr
 195 200 205

Val Pro Ser Gly Lys Gly Ser Thr Thr Pro Thr Lys Ala Gly Val Ile
 210 215 220

Leu Asn Asn Ser Glu Tyr Lys Met Leu Ile Asp Asn Gly Tyr Met Val
 225 230 235 240

His Val Asp Lys Val Ser Lys Val Val Lys Lys Gly Val Glu Cys Leu
 245 250 255

```

- 135 -

Gln Ile Glu Gly Thr Leu Lys Lys Ser Leu Asp Phe Lys Asn Asp Ile  
 260 265 270  
 Asn Ala Glu Ala His Ser Trp Gly Met Lys Asn Tyr Glu Glu Trp Ala  
 275 280 285  
 Lys Asp Leu Thr Asp Ser Gln Arg Glu Ala Leu Asp Gly Tyr Ala Arg  
 290 295 300  
 Gln Asp Tyr Lys Glu Ile Asn Asn Tyr Leu Arg Asn Gln Gly Gly Ser  
 305 310 315 320  
 Gly Asn Glu Lys Leu Asp Ala Gln Ile Lys Asn Ile Ser Asp Ala Leu  
 325 330 335  
 Gly Lys Lys Pro Ile Pro Glu Asn Ile Thr Val Tyr Arg Trp Cys Gly  
 340 345 350  
 Met Pro Glu Phe Gly Tyr Gln Ile Ser Asp Pro Leu Pro Ser Leu Lys  
 355 360 365  
 Asp Phe Glu Glu Gln Phe Leu Asn Thr Ile Lys Glu Asp Lys Gly Tyr  
 370 375 380  
 Met Ser Thr Ser Leu Ser Ser Glu Arg Leu Ala Ala Phe Gly Ser Arg  
 385 390 395 400  
 Lys Ile Ile Leu Arg Leu Gln Val Pro Lys Gly Ser Thr Gly Ala Tyr  
 405 410 415  
 Leu Ser Ala Ile Gly Gly Phe Ala Ser Glu Lys Glu Ile Leu Leu Asp  
 420 425 430  
 Lys Asp Ser Lys Tyr His Ile Asp Lys Val Thr Glu Val Ile Ile Lys  
 435 440 445  
 Gly Val Lys Arg Tyr Val Val Asp Ala Thr Leu Leu Thr Asn Ser Arg  
 450 455 460  
 Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro  
 465 470 475 480  
 Ser Asp Ile Gly Ser Thr Met Lys Thr Asn Gln Ile Ser Thr Thr Gln  
 485 490 495  
 Lys Asn Gln Gln Lys Glu Met Asp Arg Lys Gly Leu Leu Gly Tyr Tyr  
 500 505 510  
 Phe Lys Gly Lys Asp Phe Ser Asn Leu Thr Met Phe Ala Pro Thr Arg  
 515 520 525  
 Asp Ser Thr Leu Ile Tyr Asp Gln Gln Thr Ala Asn Lys Leu Leu Asp  
 530 535 540  
 Lys Lys Gln Gln Glu Tyr Gln Ser Ile Arg Trp Ile Gly Leu Ile Gln

- 136 -

545                      550                      555                      560  
 Ser Lys Glu Thr Gly Asp Phe Thr Phe Asn Leu Ser Glu Asp Glu Gln  
                                  565                                   570                                   575  
 Ala Ile Ile Glu Ile Asn Gly Lys Ile Ile Ser Asn Lys Gly Lys Glu  
                                  580                                   585                                   590  
 Lys Gln Val Val His Leu Glu Lys Gly Lys Leu Val Pro Ile Lys Ile  
                                  595                                   600                                   605  
 Glu Tyr Gln Ser Asp Thr Lys Phe Asn Ile Asp Ser Lys Thr Phe Lys  
                                  610                                   615                                   620  
 Glu Leu Lys Leu Phe Lys Ile Asp Ser Gln Asn Gln Pro Gln Gln Val  
                                  625                                   630                                   635                                   640  
 Gln Gln Asp Glu Leu Arg Asn Pro Glu Phe Asn Lys Lys Glu Ser Gln  
                                  645                                   650                                   655  
 Glu Phe Leu Ala Lys Pro Ser Lys Ile Asn Leu Phe Thr Gln Gln Met  
                                  660                                   665                                   670  
 Lys Arg Glu Ile Asp Glu Asp Thr Asp Thr Asp Gly Asp Ser Ile Pro  
                                  675                                   680                                   685  
 Asp Leu Trp Glu Glu Asn Gly Tyr Thr Ile Gln Asn Arg Ile Ala Val  
                                  690                                   695                                   700  
 Lys Trp Asp Asp Ser Leu Ala Ser Lys Gly Tyr Thr Lys Phe Val Ser  
                                  705                                   710                                   715                                   720  
 Asn Pro Leu Glu Ser His Thr Val Gly Asp Pro Tyr Thr Asp Tyr Glu  
                                  725                                   730                                   735  
 Lys Ala Ala Arg Asp Leu Asp Leu Ser Asn Ala Lys Glu Thr Phe Asn  
                                  740                                   745                                   750  
 Pro Leu Val Ala Ala Phe Pro Ser Val Asn Val Ser Met Glu Lys Val  
                                  755                                   760                                   765  
 Ile Leu Ser Pro Asn Glu Asn Leu Ser Asn Ser Val Glu Ser His Ser  
                                  770                                   775                                   780  
 Ser Thr Asn Trp Ser Tyr Thr Asn Thr Glu Gly Ala Ser Val Glu Ala  
                                  785                                   790                                   795                                   800  
 Gly Ile Gly Pro Lys Gly Ile Ser Phe Gly Val Ser Val Asn Tyr Gln  
                                  805                                   810                                   815  
 His Ser Glu Thr Val Ala Gln Glu Trp Gly Thr Ser Thr Gly Asn Thr  
                                  820                                   825                                   830  
 Ser Gln Phe Asn Thr Ala Ser Ala Gly Tyr Leu Asn Ala Asn Val Arg  
                                  835                                   840                                   845

- 137 -

Tyr Asn Asn Val Gly Thr Gly Ala Ile Tyr Asp Val Lys Pro Thr Thr  
 850 855 860  
 Ser Phe Val Leu Asn Asn Asp Thr Ile Ala Thr Ile Thr Ala Lys Ser  
 865 870 875 880  
 Asn Ser Thr Ala Leu Asn Ile Ser Pro Gly Glu Ser Tyr Pro Lys Lys  
 885 890 895  
 Gly Gln Asn Gly Ile Ala Ile Thr Ser Met Asp Asp Phe Asn Ser His  
 900 905 910  
 Pro Ile Thr Leu Asn Lys Lys Gln Val Asp Asn Leu Leu Asn Asn Lys  
 915 920 925  
 Pro Met Met Leu Glu Thr Asn Gln Thr Asp Gly Val Tyr Lys Ile Lys  
 930 935 940  
 Asp Thr His Gly Asn Ile Val Thr Gly Gly Glu Trp Asn Gly Val Ile  
 945 950 955 960  
 Gln Gln Ile Lys Ala Lys Thr Ala Ser Ile Ile Val Asp Asp Gly Glu  
 965 970 975  
 Arg Val Ala Glu Lys Arg Val Ala Ala Lys Asp Tyr Glu Asn Pro Glu  
 980 985 990  
 Asp Lys Thr Pro Ser Leu Thr Leu Lys Asp Ala Leu Lys Leu Ser Tyr  
 995 1000 1005  
 Pro Asp Glu Ile Lys Glu Ile Glu Gly Leu Leu Tyr Tyr Lys Asn Lys  
 1010 1015 1020  
 Pro Ile Tyr Glu Ser Ser Val Met Thr Tyr Leu Asp Glu Asn Thr Ala  
 1025 1030 1035 1040  
 Lys Glu Val Thr Lys Gln Leu Asn Asp Thr Thr Gly Lys Phe Lys Asp  
 1045 1050 1055  
 Val Ser His Leu Tyr Asp Val Lys Leu Thr Pro Lys Met Asn Val Thr  
 1060 1065 1070  
 Ile Lys Leu Ser Ile Leu Tyr Asp Asn Ala Glu Ser Asn Asp Asn Ser  
 1075 1080 1085  
 Ile Gly Lys Trp Thr Asn Thr Asn Ile Val Ser Gly Gly Asn Asn Gly  
 1090 1095 1100  
 Lys Lys Gln Tyr Ser Ser Asn Asn Pro Asp Ala Asn Leu Thr Leu Asn  
 1105 1110 1115 1120  
 Thr Asp Ala Gln Glu Lys Leu Asn Lys Asn Arg Asp Tyr Tyr Ile Ser  
 1125 1130 1135

- 138 -

Leu Tyr Met Lys Ser Glu Lys Asn Thr Gln Cys Glu Ile Thr Ile Asp  
 1140 1145 1150  
 Gly Glu Ile Tyr Pro Ile Thr Thr Lys Thr Val Asn Val Asn Lys Asp  
 1155 1160 1165  
 Asn Tyr Lys Arg Leu Asp Ile Ile Ala His Asn Ile Lys Ser Asn Pro  
 1170 1175 1180  
 Ile Ser Ser Leu His Ile Lys Thr Asn Asp Glu Ile Thr Leu Phe Trp  
 1185 1190 1195 1200  
 Asp Asp Ile Ser Ile Thr Asp Val Ala Ser Ile Lys Pro Glu Asn Leu  
 1205 1210 1215  
 Thr Asp Ser Glu Ile Lys Gln Ile Tyr Ser Arg Tyr Gly Ile Lys Leu  
 1220 1225 1230  
 Glu Asp Gly Ile Leu Ile Asp Lys Lys Gly Gly Ile His Tyr Gly Glu  
 1235 1240 1245  
 Phe Ile Asn Glu Ala Ser Phe Asn Ile Glu Pro Leu Gln Asn Tyr Val  
 1250 1255 1260  
 Thr Lys Tyr Glu Val Thr Tyr Ser Ser Glu Leu Gly Pro Asn Val Ser  
 1265 1270 1275 1280  
 Asp Thr Leu Glu Ser Asp Lys Ile Tyr Lys Asp Gly Thr Ile Lys Phe  
 1285 1290 1295  
 Asp Phe Thr Lys Tyr Ser Lys Asn Glu Gln Gly Leu Phe Tyr Asp Ser  
 1300 1305 1310  
 Gly Leu Asn Trp Asp Phe Lys Ile Asn Ala Ile Thr Tyr Asp Gly Lys  
 1315 1320 1325  
 Glu Met Asn Val Phe His Arg Tyr Asn Lys  
 1330 1335

## (2) INFORMATION FOR SEQ ID NO:51:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 17..2444



- 139 -

(D) OTHER INFORMATION: /product= "3A(a) synthetic:native fusion"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GGATCCACCA ATGAAC ATG AAC AAG AAC AAC ACC AAG CTG AGC ACC CGC   | 49  |
| Met Asn Lys Asn Asn Thr Lys Leu Ser Thr Arg                     |     |
| 1 5 10                                                          |     |
| GCC CTG CCG AGC TTC ATC GAC TAC TTC AAC GGC ATC TAC GGC TTC GCC | 97  |
| Ala Leu Pro Ser Phe Ile Asp Tyr Phe Asn Gly Ile Tyr Gly Phe Ala |     |
| 15 20 25                                                        |     |
| ACC GGC ATC AAG GAC ATC ATG AAC ATG ATC TTC AAG ACC GAC ACC GGC | 145 |
| Thr Gly Ile Lys Asp Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly |     |
| 30 35 40                                                        |     |
| GGC GAC CTG ACC CTG GAC GAG ATC CTG AAG AAC CAG CAG CTG CTG AAC | 193 |
| Gly Asp Leu Thr Leu Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn |     |
| 45 50 55                                                        |     |
| GAC ATC AGC GGC AAG CTG GAC GGC GTG AAC GGC AGC CTG AAC GAC CTG | 241 |
| Asp Ile Ser Gly Lys Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu |     |
| 60 65 70 75                                                     |     |
| ATC GCC CAG GGC AAC CTG AAC ACC GAG CTG AGC AAG GAG ATC CTT AAG | 289 |
| Ile Ala Gln Gly Asn Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys |     |
| 80 85 90                                                        |     |
| ATC GCC AAC GAG CAG AAC CAG GTG CTG AAC GAC GTG AAC AAC AAG CTG | 337 |
| Ile Ala Asn Glu Gln Asn Gln Val Leu Asn Asp Val Asn Asn Lys Leu |     |
| 95 100 105                                                      |     |
| GAC GCC ATC AAC ACC ATG CTG CGC GTG TAC CTG CCG AAG ATC ACC AGC | 385 |
| Asp Ala Ile Asn Thr Met Leu Arg Val Tyr Leu Pro Lys Ile Thr Ser |     |
| 110 115 120                                                     |     |
| ATG CTG AGC GAC GTG ATG AAG CAG AAC TAC GCC CTG AGC CTG CAG ATC | 433 |
| Met Leu Ser Asp Val Met Lys Gln Asn Tyr Ala Leu Ser Leu Gln Ile |     |
| 125 130 135                                                     |     |
| GAG TAC CTG AGC AAG CAG CTG CAG GAG ATC AGC GAC AAG CTG GAC ATC | 481 |
| Glu Tyr Leu Ser Lys Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Ile |     |
| 140 145 150 155                                                 |     |
| ATC AAC GTG AAC GTC CTG ATC AAC AGC ACC CTG ACC GAG ATC ACC CCG | 529 |
| Ile Asn Val Asn Val Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro |     |
| 160 165 170                                                     |     |
| GCC TAC CAG CGC ATC AAG TAC GTG AAC GAG AAG TTC GAA GAG CTG ACC | 577 |
| Ala Tyr Gln Arg Ile Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr |     |
| 175 180 185                                                     |     |
| TTC GCC ACC GAG ACC AGC AGC AAG GTG AAG AAG GAC GGC AGC CCG GCC | 625 |

- 140 -

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Phe | Ala | Thr | Glu | Thr | Ser | Ser | Lys | Val | Lys | Lys | Asp | Gly | Ser | Pro | Ala |      |
|     | 190 |     |     |     |     |     | 195 |     |     |     |     | 200 |     |     |     |      |
| GAC | ATC | CTG | GAC | GAG | CTG | ACC | GAG | CTG | ACC | GAG | CTG | GCC | AAG | AGC | GTG | 673  |
| Asp | Ile | Leu | Asp | Glu | Leu | Thr | Glu | Leu | Thr | Glu | Leu | Ala | Lys | Ser | Val |      |
|     | 205 |     |     |     |     | 210 |     |     |     |     | 215 |     |     |     |     |      |
| ACC | AAG | AAC | GAC | GTG | GAC | GGC | TTC | GAG | TTC | TAC | CTG | AAC | ACC | TTC | CAC | 721  |
| Thr | Lys | Asn | Asp | Val | Asp | Gly | Phe | Glu | Phe | Tyr | Leu | Asn | Thr | Phe | His |      |
|     | 220 |     |     |     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |      |
| GAC | GTG | ATG | GTG | GGC | AAC | AAC | CTG | TTC | GGC | CGC | AGC | GCC | CTG | AAG | ACC | 769  |
| Asp | Val | Met | Val | Gly | Asn | Asn | Leu | Phe | Gly | Arg | Ser | Ala | Leu | Lys | Thr |      |
|     |     |     |     | 240 |     |     |     |     | 245 |     |     |     |     | 250 |     |      |
| GCC | AGC | GAG | CTG | ATC | ACC | AAG | GAG | AAC | GTG | AAG | ACC | AGC | GCC | AGC | GAG | 817  |
| Ala | Ser | Glu | Leu | Ile | Thr | Lys | Glu | Asn | Val | Lys | Thr | Ser | Gly | Ser | Glu |      |
|     |     |     | 255 |     |     |     |     | 260 |     |     |     |     | 265 |     |     |      |
| GTG | GGC | AAC | GTG | TAC | AAC | TTC | CTG | ATC | GTG | CTG | ACC | GCC | CTG | CAG | GCC | 865  |
| Val | Gly | Asn | Val | Tyr | Asn | Phe | Leu | Ile | Val | Leu | Thr | Ala | Leu | Gln | Ala |      |
|     |     |     | 270 |     |     |     | 275 |     |     |     |     | 280 |     |     |     |      |
| CAG | GCC | TTC | CTG | ACC | CTG | ACC | ACC | TGT | CGC | AAG | CTG | CTG | GCC | CTG | GCC | 913  |
| Gln | Ala | Phe | Leu | Thr | Leu | Thr | Thr | Cys | Arg | Lys | Leu | Leu | Gly | Leu | Ala |      |
|     | 285 |     |     |     |     | 290 |     |     |     |     | 295 |     |     |     |     |      |
| GAC | ATC | GAC | TAC | ACC | AGC | ATC | ATG | AAC | GAG | CAC | TTG | AAC | AAG | GAG | AAG | 961  |
| Asp | Ile | Asp | Tyr | Thr | Ser | Ile | Met | Asn | Glu | His | Leu | Asn | Lys | Glu | Lys |      |
|     | 300 |     |     |     | 305 |     |     |     |     | 310 |     |     |     |     | 315 |      |
| GAG | GAG | TTC | CGC | GTG | AAC | ATC | CTG | CCG | ACC | CTG | AGC | AAC | ACC | TTC | AGC | 1009 |
| Glu | Glu | Phe | Arg | Val | Asn | Ile | Leu | Pro | Thr | Leu | Ser | Asn | Thr | Phe | Ser |      |
|     |     |     |     | 320 |     |     |     |     | 325 |     |     |     |     | 330 |     |      |
| AAC | CCG | AAC | TAC | GCC | AAG | GTG | AAG | GGC | AGC | GAC | GAG | GAC | GCC | AAG | ATG | 1057 |
| Asn | Pro | Asn | Tyr | Ala | Lys | Val | Lys | Gly | Ser | Asp | Glu | Asp | Ala | Lys | Met |      |
|     |     |     | 335 |     |     |     |     | 340 |     |     |     |     | 345 |     |     |      |
| ATC | GTG | GAG | GCT | AAG | CCG | GGC | CAC | GCG | TTG | ATC | GGC | TTC | GAG | ATC | AGC | 1105 |
| Ile | Val | Glu | Ala | Lys | Pro | Gly | His | Ala | Leu | Ile | Gly | Phe | Glu | Ile | Ser |      |
|     |     | 350 |     |     |     | 355 |     |     |     |     |     | 360 |     |     |     |      |
| AAC | GAC | AGC | ATC | ACC | GTG | CTG | AAG | GTG | TAC | GAG | GCC | AAG | CTG | AAG | CAG | 1153 |
| Asn | Asp | Ser | Ile | Thr | Val | Leu | Lys | Val | Tyr | Glu | Ala | Lys | Leu | Lys | Gln |      |
|     | 365 |     |     |     |     | 370 |     |     |     |     | 375 |     |     |     |     |      |
| AAC | TAC | CAG | GTG | GAC | AAG | GAC | AGC | TTG | AGC | GAG | GTG | ATC | TAC | GCC | GAC | 1201 |
| Asn | Tyr | Gln | Val | Asp | Lys | Asp | Ser | Leu | Ser | Glu | Val | Ile | Tyr | Gly | Asp |      |
|     | 380 |     |     |     | 385 |     |     |     |     | 390 |     |     |     |     | 395 |      |
| ATG | GAC | AAG | CTG | CTG | TGT | CCG | GAC | CAG | AGC | GAG | CAA | ATC | TAC | TAC | ACC | 1249 |
| Met | Asp | Lys | Leu | Leu | Cys | Pro | Asp | Gln | Ser | Glu | Gln | Ile | Tyr | Tyr | Thr |      |
|     |     |     |     | 400 |     |     |     |     | 405 |     |     |     |     |     | 410 |      |

- 141 -

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| AAC AAC ATC GTG TTC CCG AAC GAG TAC GTG ATC ACC AAG ATC GAC TTC<br>Asn Asn Ile Val Phe Pro Asn Glu Tyr Val Ile Thr Lys Ile Asp Phe<br>415 420 425     | 1297 |
| ACC AAG AAG ATG AAG ACC CTG CGC TAC GAG GTG ACC GCC AAC TTC TAC<br>Thr Lys Lys Met Lys Thr Leu Arg Tyr Glu Val Thr Ala Asn Phe Tyr<br>430 435 440     | 1345 |
| GAC AGC AGC ACC GGC GAG ATC GAC CTG AAC AAG AAG AAG GTG GAG AGC<br>Asp Ser Ser Thr Gly Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser<br>445 450 455     | 1393 |
| AGC GAG GCC GAG TAC CGC ACC CTG AGC GCG AAC GAC GAC GGC GTC TAC<br>Ser Glu Ala Glu Tyr Arg Thr Leu Ser Ala Asn Asp Asp Gly Val Tyr<br>460 465 470 475 | 1441 |
| ATG CCA CTG GGC GTG ATC AGC GAG ACC TTC CTG ACC CCG ATC AAC GGC<br>Met Pro Leu Gly Val Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly<br>480 485 490     | 1489 |
| TTT GGC CTG CAG GCC GAC GAG AAC AGC CGC CTG ATC ACC CTG ACC TGT<br>Phe Gly Leu Gln Ala Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys<br>495 500 505     | 1537 |
| AAG AGC TAC CTG CGC GAG CTG CTG CTA GCC ACC GAC CTG AGC AAC AAG<br>Lys Ser Tyr Leu Arg Glu Leu Leu Leu Ala Thr Asp Leu Ser Asn Lys<br>510 515 520     | 1585 |
| GAG ACC AAG CTG ATC GTG CCA CCG AGC GGC TTC ATC AGC AAC ATC GTG<br>Glu Thr Lys Leu Ile Val Pro Pro Ser Gly Phe Ile Ser Asn Ile Val<br>525 530 535     | 1633 |
| GAG AAC GGC AGC ATC GAG GAG GAC AAC CTG GAG CCG TGG AAG GCC AAC<br>Glu Asn Gly Ser Ile Glu Glu Asp Asn Leu Glu Pro Trp Lys Ala Asn<br>540 545 550 555 | 1681 |
| AAC AAG AAC GCC TAC GTG GAC CAC ACC GGC GGC GTG AAC GGC ACC AAG<br>Asn Lys Asn Ala Tyr Val Asp His Thr Gly Gly Val Asn Gly Thr Lys<br>560 565 570     | 1729 |
| GCC CTG TAC GTG CAC AAG GAC GGC GGC ATC AGC CAG TTC ATC GGC GAC<br>Ala Leu Tyr Val His Lys Asp Gly Gly Ile Ser Gln Phe Ile Gly Asp<br>575 580 585     | 1777 |
| AAG CTG AAG CCG AAG ACC GAG TAC GTG ATC CAG TAC ACC GTG AAG GGC<br>Lys Leu Lys Pro Lys Thr Glu Tyr Val Ile Gln Tyr Thr Val Lys Gly<br>590 595 600     | 1825 |
| AAG CCA TCG ATT CAC CTG AAG GAC GAG AAC ACC GGC TAC ATC CAC TAC<br>Lys Pro Ser Ile His Leu Lys Asp Glu Asn Thr Gly Tyr Ile His Tyr<br>605 610 615     | 1873 |
| GAG GAC ACC AAC AAC AAC CTG GAG GAC TAC CAG ACC ATC AAC AAG CGC<br>Glu Asp Thr Asn Asn Asn Leu Glu Asp Tyr Gln Thr Ile Asn Lys Arg<br>620 625 630 635 | 1921 |

- 142 -

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| TTC ACC ACC GGC ACC GAC CTG AAG GGC GTG TAC CTG ATC CTG AAG AGC<br>Phe Thr Thr Gly Thr Asp Leu Lys Gly Val Tyr Leu Ile Leu Lys Ser<br>640 645 650     | 1969 |
| CAG AAC GGC GAC GAG GCC TGG GGC GAC AAC TTC ATC ATC CTG GAG ATC<br>Gln Asn Gly Asp Glu Ala Trp Gly Asp Asn Phe Ile Ile Leu Glu Ile<br>655 660 665     | 2017 |
| AGC CCG AGC GAG AAG CTG CTG AGC CCG GAG CTG ATC AAC ACC AAC AAC<br>Ser Pro Ser Glu Lys Leu Leu Ser Pro Glu Leu Ile Asn Thr Asn Asn<br>670 675 680     | 2065 |
| TGG ACC AGC ACC GGC AGC ACC AAC ATC AGC GGC AAC ACC CTG ACC CTG<br>Trp Thr Ser Thr Gly Ser Thr Asn Ile Ser Gly Asn Thr Leu Thr Leu<br>685 690 695     | 2113 |
| TAC CAG GGC GGC CCG GGG ATT CTA AAA CAA AAC CTT CAA TTA GAT AGT<br>Tyr Gln Gly Gly Arg Gly Ile Leu Lys Gln Asn Leu Gln Leu Asp Ser<br>700 705 710 715 | 2161 |
| TTT TCA ACT TAT AGA GTG TAT TTT TCT GTG TCC GGA GAT GCT AAT GTA<br>Phe Ser Thr Tyr Arg Val Tyr Phe Ser Val Ser Gly Asp Ala Asn Val<br>720 725 730     | 2209 |
| AGG ATT AGA AAT TCT AGG GAA GTG TTA TTT GAA AAA AGA TAT ATG AGC<br>Arg Ile Arg Asn Ser Arg Glu Val Leu Phe Glu Lys Arg Tyr Met Ser<br>735 740 745     | 2257 |
| GGT GCT AAA GAT GTT TCT GAA ATG TTC ACT ACA AAA TTT GAG AAA GAT<br>Gly Ala Lys Asp Val Ser Glu Met Phe Thr Thr Lys Phe Glu Lys Asp<br>750 755 760     | 2305 |
| AAC TTT TAT ATA GAG CTT TCT CAA GGG AAT AAT TTA TAT GGT GGT CCT<br>Asn Phe Tyr Ile Glu Leu Ser Gln Gly Asn Asn Leu Tyr Gly Gly Pro<br>765 770 775     | 2353 |
| ATT GTA CAT TTT TAC GAT GTC TCT ATT AAG NAA GAT CCG GAT CTA ATA<br>Ile Val His Phe Tyr Asp Val Ser Ile Lys Xaa Asp Arg Asp Leu Ile<br>780 785 790 795 | 2401 |
| TTA ACA GTT TTT AAA AGC NAA TTC TTG TAT AAT GTC CTT GAT T<br>Leu Thr Val Phe Lys Ser Xaa Phe Leu Tyr Asn Val Leu Asp<br>800 805                       | 2444 |

## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

- 143 -

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Lys | Asn | Asn | Thr | Lys | Leu | Ser | Thr | Arg | Ala | Leu | Pro | Ser | Phe | 1   | 5   | 10  | 15  |
| Ile | Asp | Tyr | Phe | Asn | Gly | Ile | Tyr | Gly | Phe | Ala | Thr | Gly | Ile | Lys | Asp | 20  | 25  | 30  |     |
| Ile | Met | Asn | Met | Ile | Phe | Lys | Thr | Asp | Thr | Gly | Gly | Asp | Leu | Thr | Leu | 35  | 40  | 45  |     |
| Asp | Glu | Ile | Leu | Lys | Asn | Gln | Gln | Leu | Leu | Asn | Asp | Ile | Ser | Gly | Lys | 50  | 55  | 60  |     |
| Leu | Asp | Gly | Val | Asn | Gly | Ser | Leu | Asn | Asp | Leu | Ile | Ala | Gln | Gly | Asn | 65  | 70  | 75  | 80  |
| Leu | Asn | Thr | Glu | Leu | Ser | Lys | Glu | Ile | Leu | Lys | Ile | Ala | Asn | Glu | Gln | 85  | 90  | 95  |     |
| Asn | Gln | Val | Leu | Asn | Asp | Val | Asn | Asn | Lys | Leu | Asp | Ala | Ile | Asn | Thr | 100 | 105 | 110 |     |
| Met | Leu | Arg | Val | Tyr | Leu | Pro | Lys | Ile | Thr | Ser | Met | Leu | Ser | Asp | Val | 115 | 120 | 125 |     |
| Met | Lys | Gln | Asn | Tyr | Ala | Leu | Ser | Leu | Gln | Ile | Glu | Tyr | Leu | Ser | Lys | 130 | 135 | 140 |     |
| Gln | Leu | Gln | Glu | Ile | Ser | Asp | Lys | Leu | Asp | Ile | Ile | Asn | Val | Asn | Val | 145 | 150 | 155 | 160 |
| Leu | Ile | Asn | Ser | Thr | Leu | Thr | Glu | Ile | Thr | Pro | Ala | Tyr | Gln | Arg | Ile | 165 | 170 | 175 |     |
| Lys | Tyr | Val | Asn | Glu | Lys | Phe | Glu | Glu | Leu | Thr | Phe | Ala | Thr | Glu | Thr | 180 | 185 | 190 |     |
| Ser | Ser | Lys | Val | Lys | Lys | Asp | Gly | Ser | Pro | Ala | Asp | Ile | Leu | Asp | Glu | 195 | 200 | 205 |     |
| Leu | Thr | Glu | Leu | Thr | Glu | Leu | Ala | Lys | Ser | Val | Thr | Lys | Asn | Asp | Val | 210 | 215 | 220 |     |
| Asp | Gly | Phe | Glu | Phe | Tyr | Leu | Asn | Thr | Phe | His | Asp | Val | Met | Val | Gly | 225 | 230 | 235 | 240 |
| Asn | Asn | Leu | Phe | Gly | Arg | Ser | Ala | Leu | Lys | Thr | Ala | Ser | Glu | Leu | Ile | 245 | 250 | 255 |     |
| Thr | Lys | Glu | Asn | Val | Lys | Thr | Ser | Gly | Ser | Glu | Val | Gly | Asn | Val | Tyr | 260 | 265 | 270 |     |
| Asn | Phe | Leu | Ile | Val | Leu | Thr | Ala | Leu | Gln | Ala | Gln | Ala | Phe | Leu | Thr | 275 | 280 | 285 |     |

- 144 -

Leu Thr Thr Cys Arg Lys Leu Leu Gly Leu Ala Asp Ile Asp Tyr Thr  
 290 295 300  
 Ser Ile Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe Arg Val  
 305 310 315 320  
 Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Ala  
 325 330 335  
 Lys Val Lys Gly Ser Asp Glu Asp Ala Lys Met Ile Val Glu Ala Lys  
 340 345 350  
 Pro Gly His Ala Leu Ile Gly Phe Glu Ile Ser Asn Asp Ser Ile Thr  
 355 360 365  
 Val Leu Lys Val Tyr Glu Ala Lys Leu Lys Gln Asn Tyr Gln Val Asp  
 370 375 380  
 Lys Asp Ser Leu Ser Glu Val Ile Tyr Gly Asp Met Asp Lys Leu Leu  
 385 390 395 400  
 Cys Pro Asp Gln Ser Glu Gln Ile Tyr Tyr Thr Asn Asn Ile Val Phe  
 405 410 415  
 Pro Asn Glu Tyr Val Ile Thr Lys Ile Asp Phe Thr Lys Lys Met Lys  
 420 425 430  
 Thr Leu Arg Tyr Glu Val Thr Ala Asn Phe Tyr Asp Ser Ser Thr Gly  
 435 440 445  
 Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser Ser Glu Ala Glu Tyr  
 450 455 460  
 Arg Thr Leu Ser Ala Asn Asp Asp Gly Val Tyr Met Pro Leu Gly Val  
 465 470 475 480  
 Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Leu Gln Ala  
 485 490 495  
 Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys Lys Ser Tyr Leu Arg  
 500 505 510  
 Glu Leu Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys Leu Ile  
 515 520 525  
 Val Pro Pro Ser Gly Phe Ile Ser Asn Ile Val Glu Asn Gly Ser Ile  
 530 535 540  
 Glu Glu Asp Asn Leu Glu Pro Trp Lys Ala Asn Asn Lys Asn Ala Tyr  
 545 550 555 560  
 Val Asp His Thr Gly Gly Val Asn Gly Thr Lys Ala Leu Tyr Val His  
 565 570 575

- 145 -

Lys Asp Gly Gly Ile Ser Gln Phe Ile Gly Asp Lys Leu Lys Pro Lys  
 580 585 590  
 Thr Glu Tyr Val Ile Gln Tyr Thr Val Lys Gly Lys Pro Ser Ile His  
 595 600 605  
 Leu Lys Asp Glu Asn Thr Gly Tyr Ile His Tyr Glu Asp Thr Asn Asn  
 610 615 620  
 Asn Leu Glu Asp Tyr Gln Thr Ile Asn Lys Arg Phe Thr Thr Gly Thr  
 625 630 635 640  
 Asp Leu Lys Gly Val Tyr Leu Ile Leu Lys Ser Gln Asn Gly Asp Glu  
 645 650 655  
 Ala Trp Gly Asp Asn Phe Ile Ile Leu Glu Ile Ser Pro Ser Glu Lys  
 660 665 670  
 Leu Leu Ser Pro Glu Leu Ile Asn Thr Asn Asn Trp Thr Ser Thr Gly  
 675 680 685  
 Ser Thr Asn Ile Ser Gly Asn Thr Leu Thr Leu Tyr Gln Gly Gly Arg  
 690 695 700  
 Gly Ile Leu Lys Gln Asn Leu Gln Leu Asp Ser Phe Ser Thr Tyr Arg  
 705 710 715 720  
 Val Tyr Phe Ser Val Ser Gly Asp Ala Asn Val Arg Ile Arg Asn Ser  
 725 730 735  
 Arg Glu Val Leu Phe Glu Lys Arg Tyr Met Ser Gly Ala Lys Asp Val  
 740 745 750  
 Ser Glu Met Phe Thr Thr Lys Phe Glu Lys Asp Asn Phe Tyr Ile Glu  
 755 760 765  
 Leu Ser Gln Gly Asn Asn Leu Tyr Gly Gly Pro Ile Val His Phe Tyr  
 770 775 780  
 Asp Val Ser Ile Lys Xaa Asp Arg Asp Leu Ile Leu Thr Val Phe Lys  
 785 790 795 800  
 Ser Xaa Phe Leu Tyr Asn Val Leu Asp  
 805

- 146 -

## (2) INFORMATION FOR SEQ ID NO:53:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3474 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: ~~linear~~

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Pure maize optimized synthetic BT CryIA(b) gene

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ATGGACAACA ACCCCAACAT CAACGAGTGC ATCCCCTACA ACTGCCTGAG CAACCCCGAG  
60

GTGGAGGTGC TGGGCGGCGA GCGCATCGAG ACCGGCTACA CCCCATCGA CATCAGCCTG  
120

AGCCTGACCC AGTTCCTGCT GAGCGAGTTC GTGCCC GGCG CCGGCTTCGT GCTGGGCCTG  
180

GTGGACATCA TCTGGGGCAT CTCGGGCCCC AGCCAGTGGG ACGCCTTCCT GGTGCAGATC  
240

GAGCAGCTGA TCAACCAGCG CATCGAGGAG TTCGCCC GCA ACCAGGCCAT CAGCCGCCTG  
300

GAGGGCCTGA GCAACCTGTA CCAGATCTAC GCCGAGAGCT TCCGCGAGTG GGAGGCCGAC  
360



- 147 -

CCCACCAACC CCGCCCTGCG CGAGGAGATG CGCATCCAGT TCAACGACAT GAACAGCGCC  
420

CTGACCACCG CCATCCCCCT GTTCGCCGTG CAGAACTACC AGGTGCCCCCT GCTGAGCGTG  
480

TACGTGCAGG CCGCCAACCT GCACCTGAGC GTGCTGCGCG ACGTGAGCGT GTTCGGCCAG  
540

CGCTGGGGCT TCGACGCCGC CACCATCAAC AGCCGCTACA ACGACCTGAC CCGCCTGATC  
600

GGCAACTACA CCGACCACGC CGTGCGCTGG TACAACACCG GCCTGGAGCG CGTGTGGGGC  
660

CCCGACAGCC GCGACTGGAT CCGCTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG  
720

CTGGACATCG TGAGCCTGTT CCCCAACTAC GACAGCCGCA CCTACCCCAT CCGCACCCTG  
780

AGCCAGCTGA CCCGCGAGAT CTACACCAAC CCCGTGCTGG AGAACTTCGA CGGCAGCTTC  
840

CGCGGCAGCG CCCAGGGCAT CGAGGGCAGC ATCCGCAGCC CCCACCTGAT GGACATCCTG  
900

AACAGCATCA CCATCTACAC CGACGCCCAC CGCGGCGAGT ACTACTGGAG CGGCCACCAG  
960

ATCATGGCCA GCCCCGTGGG CTTACGCGGC CCCGAGTTCA CCTTCCCCCT GTACGGCACC  
1020

ATGGGCAACG CCGCCCCCA GCAGCGCATC GTGGCCCAGC TGGGCCAGGG CGTGTACCGC  
1080

- 148 -

ACCCTGAGCA GCACCCTGTA CCGCCGCCCC TTCAACATCG GCATCAACAA CCAGCAGCTG  
1140

AGCGTGCTGG ACGGCACCGA GTTCGCCTAC GGCACCAGCA GCAACCTGCC CAGCGCCGTG  
1200

TACCGCAAGA GCGGCACCGT GGACAGCCTG GACGAGATCC CCCCCAGAA CAACAACGTG  
1260

CCCCCCGCC AGGGCTTCAG CCACCGCCTG AGCCACGTGA GCATGTTCCG CAGCGGCTTC  
1320

AGCAACAGCA GCGTGAGCAT CATCCGCGCC CCCATGTTCA GCTGGATCCA CCGCAGCGCC  
1380

GAGTTCAACA ACATCATCCC CAGCAGCCAG ATCACCAGCA TCCCCCTGAC CAAGAGCACC  
1440

AACCTGGGCA GCGGCACCAG CGTGGTGAAG GGCCCCGGCT TCACCGGCGG CGACATCCTG  
1500

CGCCGCACCA GCCCCGGCCA GATCAGCACC CTGCGCGTGA ACATCACCGC CCCCCTGAGC  
1560

CAGCGCTACC GCGTGCGCAT CCGCTACGCC AGCACCACCA ACCTGCAGTT CCACACCAGC  
1620

ATCGACGGCC GCCCCATCAA CCAGGGCAAC TTCAGCGCCA CCATGAGCAG CGGCAGCAAC  
1680

CTGCAGAGCG GCAGCTTCCG CACCGTGGGC TTCACCACCC CCTTCAACTT CAGCAACGGC  
1740

AGCAGCGTGT TCACCCTGAG CGCCCACGTG TTCAACAGCG GCAACGAGGT GTACATCGAC  
1800

- 149 -

CGCATCGAGT TCGTGCCCGC CGAGGTGACC TTCGAGGCCG AGTACGACCT GGAGCGCGCC  
1860

CAGAAGGCCG TGAACGAGCT GTTCACCAGC AGCAACCAGA TCGGCCTGAA GACCGACGTG  
1920

ACCGACTACC ACATCGACCA GGTGAGCAAC CTGGTGGAGT GCCTGAGCGA CGAGTTCTGC  
1980

CTGGACGAGA AGAAGGAGCT GAGCGAGAAG GTGAAGCACG CCAAGCGCCT GAGCGACGAG  
2040

CGCAACCTGC TGCAGGACCC CAACTTCCGC GGCATCAACC GCCAGCTGGA CCGCGGCTGG  
2100

CGCGGCAGCA CCGACATCAC CATCCAGGGC GGCGACGACG TGTTCAGGA GAACTACGTG  
2160

ACCTTGCTGG GCACCTTCGA CGAGTGCTAC CCCACCTACC TGTACCAGAA GATCGACGAG  
2220

AGCAAGCTGA AGGCCTACAC CCGCTACCAG CTGCGCGGCT ACATCGAGGA CAGCCAGGAC  
2280

CTGGAGATCT ACCTGATCCG CTACAACGCC AAGCACGAGA CCGTGAACGT GCCC GGACAC  
2340

GGCAGCCTGT GGCCCCTGAG CGCCCCCAGC CCCATCGGCA AGTGCGCCCA CCACAGCCAC  
2400

CACTTCAGCC TGGACATCGA CGTGGGCTGC ACCGACCTGA ACGAGGACCT GGGCGTGTGG  
2460

GTGATCTTCA AGATCAAGAC CCAGGACGGC CACGCCCCGC TGGGCAACCT GGAGTTCCTG  
2520

- 150 -

GAGGAGAAGC CCCTGGTGGG CGAGGCCCTG GCCCGCGTGA AGCGCGCCGA GAAGAAGTGG  
2580

CGCGACAAGC GCGAGAAGCT GGAGTGGGAG ACCAACATCG TGTACAAGGA GGCCAAGGAG  
2640

AGCGTGGACG CCCTGTTCGT GAACAGCCAG TACGACCGCC TGCAGGCCGA CACCAACATC  
2700

GCCATGATCC ACGCCGCCGA CAAGCGCGTG CACAGCATCC GCGAGGCCTA CCTGCCCCGAG  
2760

CTGAGCGTGA TCCCCGGCGT GAACGCCGCC ATCTTCGAGG AGCTGGAGGG CCGCATCTTC  
2820

ACCGCCTTCA GCCTGTACGA CGCCCGCAAC GTGATCAAGA ACGGCGACTT CAACAACGGC  
2880

CTGAGCTGCT GGAACGTGAA GGGCCACGTG GACGTGGAGG AGCAGAACAA CCACCGCAGC  
2940

GTGCTGGTGG TGCCCGAGTG GGAGGCCGAG GTGAGCCAGG AGGTGCGCGT GTGCCCCGGC  
3000

CGCGGCTACA TCCTGCGCGT GACCGCCTAC AAGGAGGGCT ACGGCGAGGG CTGCGTGACC  
3060

ATCCACGAGA TCGAGAACAA CACCGACGAG CTGAAGTTCA GCAACTGCGT GGAGGAGGAG  
3120

GTGTACCCCA ACAACACCGT GACCTGCAAC GACTACACCG CCACCCAGGA GGAGTACGAG  
3180

GGCACCTACA CCAGCCGCAA CCGCGGCTAC GACGGCGCCT ACGAGAGCAA CAGCAGCGTG  
3240

- 151 -

CCCGCCGACT ACGCCAGCGC CTACGAGGAG AAGGCCTACA CCGACGGCCG CCGCGACAAC  
3300

CCCTGCGAGA GCAACCGCGG CTACGGCGAC TACACCCCCC TGCCCGCCGG CTACGTGACC  
3360

AAGGAGCTGG AGTACTTCCC CGAGACCGAC AAGGTGTGGA TCGAGATCGG CGAGACCGAG  
3420

GGCACCTTCA TCGTGGACAG CGTGGAGCTG CTGCTGATGG AGGAGTAGTA CATG  
3474

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3508 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Full length synthetic maize optimized BT CryIA(b)  
gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GATCCAACAA TGGACAACAA CCCCAACATC AACGAGTGCA TCCCCTACAA CTGCCTGAGC  
60

AACCCCGAGG TGGAGGTGCT GGGCGGCGAG CGCATCGAGA CCGGCTACAC CCCCATCGAC  
120

ATCAGCCTGA GCCTGACCCA GTTCCTGCTG AGCGAGTTCG TGCCCGGCGC CGGCTTCGTG  
180

- 152 -

CTGGGCCTGG TGGACATCAT CTGGGGCATC TTCGGCCCCA GCCAGTGGGA CGCCTTCCTG  
240

GTGCAGATCG AGCAGCTGAT CAACCAGCGC ATCGAGGAGT TCGCCCGCAA CCAGGCCATC  
300

AGCCGCCTGG AGGGCCTGAG CAACCTGTAC CAAATCTACG CCGAGAGCTT CCGCGAGTGG  
360

GAGGCCGACC CCACCAACCC CGCCCTGCGC GAGGAGATGC GCATCCAGTT CAACGACATG  
420

AACAGCGCCC TGACCACCGC CATCCCCCTG TTCGCCGTGC AGAACTACCA GGTGCCCCCTG  
480

CTGAGCGTGT ACGTGCAGGC CGCCAACCTG CACCTGAGCG TGCTGCGCGA CGTCAGCGTG  
540

TTCGGCCAGC GCTGGGGCTT CGACGCCGCC ACCATCAACA GCCGCTACAA CGACCTGACC  
600

CGCCTGATCG GCAACTACAC CGACCACGCC GTGCGCTGGT ACAACACCGG CCTGGAGCGC  
660

GTGTGGGGTC CCGACAGCCG CGACTGGATC AGGTACAACC AGTTCCGCCG CGAGCTGACC  
720

CTGACCGTGC TGGACATCGT GAGCCTGTTC CCCAACTACG ACAGCCGCAC CTACCCCATC  
780

CGCACCGTGA GCCAGCTGAC CCGCGAGATT TACACCAACC CCGTGCTGGA GAACTTCGAC  
840

GGCAGCTTCC GCGGCAGCGC CCAGGGCATC GAGGGCAGCA TCCGCAGCCC CCACCTGATG  
900

- 153 -

GACATCCTGA ACAGCATCAC CATCTACACC GACGCCCACC GCGGCGAGTA CTACTGGAGC  
960

GGCCACCAGA TCATGGCCAG CCCCCTCGGC TTCAGCGGCC CCGAGTTCAC CTTCCCCCTG  
1020

TACGGCACCA TGGGCAACGC TGCACCTCAG CAGCGCATCG TGGCACAGCT GGGCCAGGGA  
1080

GTGTACCGCA CCCTGAGCAG CACCCTGTAC CGTCGACCTT TCAACATCGG CATCAACAAC  
1140

CAGCAGCTGA GCGTGCTGGA CGGCACCGAG TTCGCCTACG GCACCAGCAG CAACCTGCCC  
1200

AGCGCCGTGT ACCGCAAGAG CGGCACCGTG GACAGCCTGG ACGAGATCCC CCCTCAGAAC  
1260

AACAACGTGC CACCTCGACA GGGCTTCAGC CACCGTCTGA GCCACGTGAG CATGTTCCGC  
1320

AGTGGCTTCA GCAACAGCAG CGTGAGCATC ATCCGTGCAC CTATGTTTAC CTGGATTAC  
1380

CGCAGTGCCG AGTTCAACAA CATCATCCCC AGCAGCCAGA TCACCCAGAT CCCCCTGACC  
1440

AAGAGCACCA ACCTGGGCAG CGGCACCAGC GTGGTGAAGG GCCCCGGCTT CACCGGCGGC  
1500

GACATCCTGC GCCGCACCAG CCCC GGCCAG ATCAGCACCC TGCGCGTGAA CATCACCGCC  
1560

CCCCTGAGCC AGCGCTACCG CGTCCGCATC CGCTACGCCA GCACCACCAA CCTGCAGTTC  
1620

- 154 -

CACACCAGCA TCGACGGCCG CCCCATCAAC CAGGGCAACT TCAGCGCCAC CATGAGCAGC  
1680

GGCAGCAACC TGCAGAGCGG CAGCTTCCGC ACCGTGGGCT TCACCACCCC CTTCAACTTC  
1740

AGCAACGGCA GCAGCGTGTT CACCCTGAGC GCCCAGGTGT TCAACAGCGG CAACGAGGTG  
1800

TACATCGACC GCATCGAGTT CGTGCCCGCC GAGGTGACCT TCGAGGCCGA GTACGACCTG  
1860

GAGAGGGCTC AGAAGGCCGT GAACGAGCTG TTCACCAGCA GCAACCAGAT CGGCCTGAAG  
1920

ACCGACGTGA CCGACTACCA CATCGATCAG GTGAGCAACC TGGTGGAGTG CCTGAGCGAC  
1980

GAGTTCTGCC TGGACGAGAA GAAGGAGCTG AGCGAGAAGG TGAAGCACGC CAAGCGCCTG  
2040

AGCGACGAGC GCAACCTGCT GCAGGACCCC AACTTCCGCG GCATCAACCG CCAGCTGGAC  
2100

CGCGGCTGGC GCGGCAGCAC CGACATCACC ATCCAGGGCG GCGACGACGT GTTCAAGGAG  
2160

AACTACGTGA CCCTGCTGGG CACCTTCGAC GAGTGCTACC CCACCTACCT GTACCAGAAG  
2220

ATCGACGAGA GCAAGCTGAA GGCCTACACC CGCTACCAGC TGC GCGGCTA CATCGAGGAC  
2280

AGCCAGGACC TGGAGATCTA CCTGATCCGC TACAACGCCA AGCACGAGAC CGTGAACGTG  
2340



- 155 -

CCCGGCACCG GCAGCCTGTG GCCCCTGAGC GCCCCCAGCC CCATCGGCAA GTGCGCCCAC  
2400

CACAGCCACC ACTTCAGCCT GGACATCGAC GTGGGCTGCA CCGACCTGAA CGAGGACCTG  
2460

GGCGTGTTGGG TGATCTTCAA GATCAAGACC CAGGACGGCC ACGCCCGCCT GGGCAACCTG  
2520

GAGTTCCTGG AGGAGAAGCC CCTGGTGGGC GAGGCCCTGG CCCGCGTGAA GCGCGCCGAG  
2580

AAGAAGTGGC GCGACAAGCG CGAGAAGCTG GAGTGGGAGA CCAACATCGT GTACAAGGAG  
2640

GCCAAGGAGA GCGTGGACGC CCTGTTCGTG AACAGCCAGT ACGACCGCCT GCAGGCCGAC  
2700

ACCAACATCG CCATGATCCA CGCCGCCGAC AAGCGCGTGC ACAGCATTCG CGAGGCCTAC  
2760

CTGCCCCGAGC TGAGCGTGAT CCCC GGCGTG AACGCCGCCA TCTTCGAGGA GCTGGAGGGC  
2820

CGCATCTTCA CCGCCTTCAG CCTGTACGAC GCCCGCAACG TGATCAAGAA CGGCGACTTC  
2880

AACAACGGCC TGAGCTGCTG GAACGTGAAG GGCCACGTGG ACGTGGAGGA GCAGAACAAC  
2940

CACCGCAGCG TGCTGGTGGT GCCCAGTGG GAGGCCGAGG TGAGCCAGGA GGTGCGCGTG  
3000

TGCCCCGGCC GCGGCTACAT CCTGCGCGTG ACCGCCTACA AGGAGGGCTA CGGCGAGGGC  
3060

- 156 -

TGCGTGACCA TCCACGAGAT CGAGAACAAC ACCGACGAGC TCAAGTTCAG CAACTGCGTG  
3120

GAGGAGGAGG TGTACCCCAA CAACACCGTG ACCTGCAACG ACTACACCGC CACCCAGGAG  
3180

GAGTACGAGG GCACCTACAC CAGCCGCAAC CGCGGCTACG ACGGCGCCTA CGAGAGCAAC  
3240

AGCAGCGTGC CCGCCGACTA CGCCAGCGCC TACGAGGAGA AGGCCTACAC CGACGGCCGC  
3300

CGCGACAACC CCTGCGAGAG CAACCGCGGC TACGGCGACT ACACCCCCCT GCCC GCCGGC  
3360

TACGTGACCA AGGAGCTGGA GTACTTCCCC GAGACCGACA AGGTGTGGAT CGAGATCGGC  
3420

GAGACCGAGG GCACCTTCAT CGTGGACAGC GTGGAGCTGC TGCTGATGGA GGAGTAGTAC  
3480

ATGTGATAGT ACGTAAGCTC GAGGATCT 3508

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1961 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

- 157 -

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Truncated synthetic maize optimized BT  
CryIA(b) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GATCCAACAA TGGACAACAA CCCCAACATC AACGAGTGCA TCCCCTACAA CTGCCTGAGC | 60  |
| AACCCCGAGG TGGAGGTGCT GGGGGGCGAG CGCATCGAGA CCGGCTACAC CCCCATCGAC | 120 |
| ATCAGCCTGA GCCTGACCCA GTTCTGTCTG AGCGAGTTCG TGCCCGGCGC CGGCTTCGTG | 180 |
| CTGGGCCTGG TGGACATCAT CTGGGGCATC TTCGGCCCCA GCCAGTGGGA CGCCTTCCTG | 240 |
| GTGCAGATCG AGCAGCTGAT CAACCAGCGC ATCGAGGAGT TCGCCCGCAA CCAGGCCATC | 300 |
| AGCCGCCTGG AGGGCCTGAG CAACCTGTAC CAAATCTACG CCGAGAGCTT CCGCGAGTGG | 360 |
| GAGGCGGACC CCACCAACCC CGCCCTGCGC GAGGAGATGC GCATCCAGTT CAACGACATG | 420 |
| AACAGCGCCC TGACCACCGC CATCCCCCTG TTCGCCGTGC AGAACTACCA GGTGCCCTG  | 480 |
| CTGAGCGTGT ACGTGCAGGC CGCCAACCTG CACCTGAGCG TGCTGCGCGA CGTCAGCGTG | 540 |
| TTCGGCCAGC GCTGGGGCTT CGACGCGGCC ACCATCAACA GCCGCTACAA CGACCTGACC | 600 |
| CGCCTGATCG GCAACTACAC CGACCAGGCC GTGCGCTGGT ACAACACCGG CCTGGAGCGC | 660 |
| GTGTGGGGTC CCGACAGCCG CGACTGGATC AGGTACAACC AGTTCCGCCG CGAGCTGACC | 720 |
| CTGACCGTGC TGGACATGTT GAGCCTGTTC CCCAACTACG ACAGCCGCAC CTACCCCATC | 780 |
| CGCACCGTGA GCCAGCTGAC CCGCGAGATT TACACCAACC CCGTGCTGGA GAACTTCGAC | 840 |

- 158 -

GGCAGCTTCC GCGGCAGGCG CCAGGGCATC GAGGGCAGCA TCCGCAGCCC CCACCTGATG 900  
GACATCCTGA ACAGCATCAC CATCTACACC GACGCCACC GCGGCGAGTA CTA CTGAGAGC 960  
GGCCACCAGA TCATGGCCAG CCGGTCGGC TTCAGCGGCC CCGAGTTCAC CTTCCCCCTG 1020  
TACGGCACCA TGGGCAACGC TGCACCTCAG CAGCGCATCG TGGCACAGCT GGGCCAGGGA 1080  
GTGTACCGCA CCCTGAGCAG CACCTGTAC CGTCGACCTT TCAACATCGG CATCAACAAC 1140  
CAGCAGCTGA GCGTGCTGGA CGGCACCGAG TTCGCCTACG GCACCAGCAG CAACCTGCCC 1200  
AGCGCCGTGT ACCGCAAGAG CGGCACCGTG GACAGCCTGG ACGAGATCCC CCTCAGAAC 1260  
AACAACTGTC CACCTGACA GGGCTTCAGC CACCGTCTGA GCCACGTGAG CATGTTCCGC 1320  
AGTGGCTTCA GCAACAGCAG CGTGAGCATC ATCCGTGCAC CTATGTTTCTAG CTGGATTCTC 1380  
CGCAGTGCCG AGTTCAACAA CATCATCCCC AGCAGCCAGA TCACCCAGAT CCCCCTGACC 1440  
AAGAGCACCA ACCTGGGCAG CGGCACCAGC GTGGTGAAGG GCGGCGGCTT CACCGGCGGC 1500  
GACATCCTGC GCGGCACCAG CCGGCGCCAG ATCAGCACCC TGCGCGTGAA CATCACCGCC 1560  
CCCCTGAGCC AGCGCTACCG CGTCGCGATC CGCTACGCCA GCACCACCAA CCTGCAGTTC 1620  
CACACCAGCA TCAGCGGCCG CCCCATCAAC CAGGGCAACT TCAGCGCCAC CATGAGCAGC 1680  
GGCAGCAACC TGCAAGAGCGG CAGCTTCCGC ACCGTGGGCT TCACCACCCC CTTCAACTTC 1740  
AGCAACGGCA GCAGCGTGT CACCTGAGC GCCACGTGT TCAACAGCGG CAACGAGGTG 1800  
TACATCGACC GCATCGAGTT CGTGCCCGCC GAGGTGACCT TCGAGGCCGA GTACGACCTG 1860  
GAGAGGGCTC AGAAGGCCGT GAACGAGCTG TTCACCAGCA GCAACCAGAT CGGCCTGAAG 1920  
ACCGACGTGA CCGACTACCA CATCGATCAG GTGTAGGAGC T 1961

**DEPOSITS**

with the Agricultural Research Service, Patent Culture Collection (NRRL), Northern Regional Research Center, 1815 North University Street, Peoria, Illinois 61604, U.S.A.

| Strain designation               | Deposition Number | Deposition Date    |
|----------------------------------|-------------------|--------------------|
| <i>Bacillus cereus</i> AB78      | NRRL B-21058      | March 18, 1998     |
| <i>Escherichia coli</i> pCIB4431 | NRRL B-18998      | September 21, 1992 |

BUDAPEST TREATY ON THE INTERNATIONAL  
RECOGNITION OF THE DEPOSIT OF MICROORGANISMS  
FOR THE PURPOSE OF PATENT PROCEDURES

## INTERNATIONAL FORM

TO

Ciba-Geigy Corp.

3054 Cornwallis Road  
Research Triangle Park, NC 27709NAME AND ADDRESS  
OF DEPOSITORRECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT  
issued pursuant to Rule 7.1 by the  
INTERNATIONAL DEPOSITARY AUTHORITY  
identified at the bottom of this page

## I. IDENTIFICATION OF THE MICROORGANISM

Identification reference given by the  
DEPOSITOR:*Escherichia coli*  
PCBI4431Accession number given by the  
INTERNATIONAL DEPOSITARY AUTHORITY:

NRRL B-18998

## II. SCIENTIFIC DESCRIPTION AND/OR PROPOSED TAXONOMIC DESIGNATION

The microorganism identified under I. above was accompanied by:

- ☐ a scientific description  
☒ a proposed taxonomic designation

(Mark with a cross where applicable)

## III. RECEIPT AND ACCEPTANCE

This International Depositary Authority accepts the microorganism identified under I.  
above, which was received by it on September 21, 1992 (date of the original deposit)<sup>1</sup>

## IV. RECEIPT OF REQUEST FOR CONVERSION

The microorganism identified under I. above was received by this International  
Depositary Authority on (date of the original deposit) and  
a request to convert the original deposit to a deposit under the Budapest Treaty  
was received by it on (date of receipt of request for conversion)

## V. INTERNATIONAL DEPOSITARY AUTHORITY

Name: Agricultural Research Culture  
Collection (NRRL)  
International Depositary Authority  
Address: 1815 N. University Street  
Peoria, Illinois 61604 U.S.A.Signature(s) of person(s) having the power  
to represent the International Depositary  
Authority or of authorized official(s):

Date:

*J. L. Suggs*  
3-20-94Where Rule 6.4(d) applies, such date is the date on which the status of international  
depositary authority was acquired.

BUDAPEST TREATY OF THE INTERNATIONAL RECOGNITION OF PATENT RIGHTS  
OF MICROORGANISMS FOR THE PURPOSE OF PATENT PROC. JRE

## INTERNATIONAL FORM

TO

Ciba-Geigy Corp.

3054 Cornwallis Road

Research Triangle Park, NC 27709

VIABILITY STATEMENT

issued pursuant to Rule 10.2 by the  
INTERNATIONAL DEPOSITARY AUTHORITY  
identified at the bottom of this page

NAME AND ADDRESS OF THE PARTY TO WHOM  
THE VIABILITY STATEMENT IS ISSUED

|                                                                                                                                                                                                                                                                  |                                                                                                                                                                                                                                                                                                                                                                                                                        |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| I. DEPOSITOR                                                                                                                                                                                                                                                     | II. IDENTIFICATION OF THE MICROORGANISM                                                                                                                                                                                                                                                                                                                                                                                |
| <p>Name: Ciba-Geigy Corp.</p> <p>Address: 3054 Cornwallis Road<br/>Research Triangle Park, NC 27709</p>                                                                                                                                                          | <p>Depositor's taxonomic designation and accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY:</p> <p><i>Escherichia coli</i> NRRL B-18998</p> <p>Date of: September 21, 1992<sup>1</sup></p> <p><input checked="" type="checkbox"/> <sup>2</sup> Original Deposit<br/> <input type="checkbox"/> <sup>2</sup> New Deposit<br/> <input type="checkbox"/> <sup>2</sup> Repropagation of Original Deposit</p> |
| III. (a) VIABILITY STATEMENT                                                                                                                                                                                                                                     |                                                                                                                                                                                                                                                                                                                                                                                                                        |
| <p>Deposit was found: <input checked="" type="checkbox"/> Viable <input type="checkbox"/> Nonviable on September 23, 1992 (Date)<br/>         International Depository Authority's preparation was found viable on October 3, 1992 (Date)<sup>3</sup></p>        |                                                                                                                                                                                                                                                                                                                                                                                                                        |
| III. (b) DEPOSITOR'S EQUIVALENCY DECLARATION                                                                                                                                                                                                                     |                                                                                                                                                                                                                                                                                                                                                                                                                        |
| <p>Depositor determined the International Depository Authority's preparation was</p> <p><input type="checkbox"/> <sup>2</sup> Equivalent <input type="checkbox"/> <sup>2</sup> Not equivalent to deposit on _____ (Date)</p> <p>Signature of Depositor _____</p> |                                                                                                                                                                                                                                                                                                                                                                                                                        |
| IV. CONDITIONS UNDER WHICH THE VIABILITY TEST WAS PERFORMED (Depositors/Depository) <sup>4</sup>                                                                                                                                                                 |                                                                                                                                                                                                                                                                                                                                                                                                                        |
|                                                                                                                                                                                                                                                                  |                                                                                                                                                                                                                                                                                                                                                                                                                        |
| V. INTERNATIONAL DEPOSITARY AUTHORITY                                                                                                                                                                                                                            |                                                                                                                                                                                                                                                                                                                                                                                                                        |
| <p>Name: Agricultural Research Culture Collection (NRRL)<br/>International Depository Authority</p> <p>Address: 1815 N. University Street<br/>Peoria, Illinois 61604 U.S.A.</p>                                                                                  | <p>Signature(s) of person(s) having the power to represent the International Depository Authority or of authorized official(s):</p> <p>Date: <i>J. J. [Signature]</i><br/>7-28-94</p>                                                                                                                                                                                                                                  |

Indicate the date of the original deposit or when a new deposit has been made.

Mark with a cross the applicable box.

In the cases referred to in Rule 10.2(a)(ii) and (iii), refer to the most recent viability test.

Fill in if the information has been requested.

-162-

**BUDAPEST TREATY ON THE INTERNATIONAL  
COGNITION OF THE DEPOSIT OF MICROORGANISMS  
FOR THE PURPOSES OF PATENT PROCEDURE**

**INTERNATIONAL FORM**

TO

Ciba-Geigy Corp.

3054 Cornwallis Road

Research Triangle Park, NC 27709

**RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT**  
issued pursuant to Rule 7.1 by the  
**INTERNATIONAL DEPOSITARY AUTHORITY**  
identified at the bottom of this page

NAME AND ADDRESS  
OF DEPOSITOR

|                                                                                                                                                                                                                                                                                                                  |                                                                                                                                                                                 |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>I. IDENTIFICATION OF THE MICROORGANISM</b>                                                                                                                                                                                                                                                                    |                                                                                                                                                                                 |
| Identification reference given by the<br>DEPOSITOR:<br><br><u>Bacillus cereus</u><br>AB78                                                                                                                                                                                                                        | Accession number given by the<br>INTERNATIONAL DEPOSITARY AUTHORITY:<br><br>NRRL B-21058                                                                                        |
| <b>II. SCIENTIFIC DESCRIPTION AND/OR PROPOSED TAXONOMIC DESIGNATION</b>                                                                                                                                                                                                                                          |                                                                                                                                                                                 |
| The microorganism identified under I above was accompanied by:<br><br><input type="checkbox"/> a scientific description<br><input checked="" type="checkbox"/> a proposed taxonomic designation<br><br>(Mark with a cross where applicable)                                                                      |                                                                                                                                                                                 |
| <b>III. RECEIPT AND ACCEPTANCE</b>                                                                                                                                                                                                                                                                               |                                                                                                                                                                                 |
| This International Depositary Authority accepts the microorganism identified under I above,<br>which was received by it on March 18, 1993 (date of the original deposit) <sup>1</sup>                                                                                                                            |                                                                                                                                                                                 |
| <b>IV. RECEIPT OF REQUEST FOR CONVERSION</b>                                                                                                                                                                                                                                                                     |                                                                                                                                                                                 |
| The microorganism identified under I above was received by this International<br>Depositary Authority on _____ (date of the original deposit) and<br>a request to convert the original deposit to a deposit under the Budapest Treaty<br>was received by it on _____ (date of receipt of request for conversion) |                                                                                                                                                                                 |
| <b>V. INTERNATIONAL DEPOSITARY AUTHORITY</b>                                                                                                                                                                                                                                                                     |                                                                                                                                                                                 |
| Name: Agricultural Research Culture<br>Collection (NRRL)<br>International Depositary Authority<br>Address: 1815 N. University Street<br>Peoria, Illinois 61604 U.S.A.                                                                                                                                            | Signature(s) of person(s) having the power<br>to represent the International Depositary<br>Authority or of authorized official(s):<br>Date: <i>J. J. [Signature]</i><br>3.24.93 |

<sup>1</sup> Where Rule 6.4(d) applies, such date is the date on which the status of international depositary authority was acquired.



-163-

**BUDAPEST TREATY ON THE INTERNATIONAL RECOGNITION OF THE DEPOSIT  
OF MICROORGANISMS FOR THE PURPOSES OF PATENT PROCEDURE**

**INTERNATIONAL FORM**

TO

Dr. Rich Lotstein  
Ciba-Geigy Corp.  
3054 Cornwallis Road  
Research Triangle Park, NC 27709

**VIABILITY STATEMENT**

issued pursuant to Rule 10.2 by the  
INTERNATIONAL DEPOSITARY AUTHORITY  
identified on the following page

NAME AND ADDRESS OF THE PARTY TO WHOM  
THE VIABILITY STATEMENT IS ISSUED

|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                                                                                                                                               |                                                                                                                                                                           |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>I. DEPOSITOR</b><br><br>Name: Ciba-Geigy Corp.<br>3054 Cornwallis Road<br>Address: Research Triangle Park, NC 27709                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | <b>II. IDENTIFICATION OF THE MICROORGANISM</b><br><br>Depositor's taxonomic designation and accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY:<br><u>Bacillus cereus</u> NRRL B-21058<br><br>Date of: <u>March 19, 1993</u><br><input checked="" type="checkbox"/> <sup>1</sup> Original Deposit<br><input type="checkbox"/> <sup>2</sup> New Deposit<br><input type="checkbox"/> <sup>3</sup> Repropagation of original deposit |                                                                                                                                                                               |                                                                                                                                                                           |
| <b>III. (a) VIABILITY STATEMENT</b><br><br>Deposit was found: <input checked="" type="checkbox"/> <sup>1</sup> Viable <input type="checkbox"/> <sup>2</sup> Nonviable on <u>March 19, 1993</u> (Date:<br>International Depository Authority's preparation was found viable on <u>March 19, 1993</u> (Date:                                                                                                                                                                                                                                                                                                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                                                                                                                                               |                                                                                                                                                                           |
| <b>III. (b) DEPOSITOR'S EQUIVALENCY DECLARATION</b><br><br>Depositor determined the International Depository Authority's preparation was<br><input checked="" type="checkbox"/> <sup>1</sup> Equivalent <input type="checkbox"/> <sup>2</sup> Not equivalent to deposit on <u>Apr. 14, 1993</u> (Date:<br>Signature of Depositor: <u>Gregory W. Warren</u>                                                                                                                                                                                                                                                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                                                                                                                                               |                                                                                                                                                                           |
| <b>IV. CONDITIONS UNDER WHICH THE VIABILITY TEST WAS PERFORMED (Depositor/Depository)<sup>4</sup></b><br><br><div style="height: 40px;"></div>                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                                                                                                                                               |                                                                                                                                                                           |
| <b>V. INTERNATIONAL DEPOSITARY AUTHORITY</b><br><br><table style="width:100%;"> <tr> <td style="width:50%;">           Name: Agricultural Research Service<br/>           Culture Collection (NRRL)<br/>           International Depository Authority<br/>           Address: 1815 N. University Street<br/>           Peoria, Illinois 61604 U.S.A.         </td> <td style="width:50%;">           Signature(s) of person(s) having the power to represent the International Depository Authority or of authorized official(s):<br/> <u>J. L. Long</u><br/>           Date: <u>3 24-93</u> </td> </tr> </table> |                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Name: Agricultural Research Service<br>Culture Collection (NRRL)<br>International Depository Authority<br>Address: 1815 N. University Street<br>Peoria, Illinois 61604 U.S.A. | Signature(s) of person(s) having the power to represent the International Depository Authority or of authorized official(s):<br><u>J. L. Long</u><br>Date: <u>3 24-93</u> |
| Name: Agricultural Research Service<br>Culture Collection (NRRL)<br>International Depository Authority<br>Address: 1815 N. University Street<br>Peoria, Illinois 61604 U.S.A.                                                                                                                                                                                                                                                                                                                                                                                                                                     | Signature(s) of person(s) having the power to represent the International Depository Authority or of authorized official(s):<br><u>J. L. Long</u><br>Date: <u>3 24-93</u>                                                                                                                                                                                                                                                                       |                                                                                                                                                                               |                                                                                                                                                                           |

<sup>1</sup>Indicate the date of the original deposit or when a new deposit has been made.

<sup>2</sup>Mark with a cross the applicable box.

<sup>3</sup>In the cases referred to in Rule 10.2(a) (ii) and (iii), refer to the most recent viability test.

<sup>4</sup>Fill in if the information has been requested.

What is claimed is:

1. A method for protecting plants including progeny thereof against damage caused by *Ostrinia furnacalis* species comprising directly or indirectly applying to the plant or the plant seed or the growing area of the plant as an active ingredient a toxin protein of *Bacillus species*.
2. A method according to claim 1, wherein the toxin protein is a toxin protein of *Bacillus thuringiensis*.
3. A method according to claim 1, wherein the toxin protein is a toxin protein of *Bacillus cereus*.
4. A method according to claim 1, wherein the toxin protein is a Cry-type protein, preferably a CryI-type protein, more preferably a CryIA-type protein, and most preferably a CryIA(b) protein.
5. A method according to claim 4, wherein the toxin protein is a CryI-type protein according to SEQ ID Nos. 53 to 55.
6. A method according to claim 1, wherein the toxin protein is a VIP-type protein, preferably a VIP1-type protein, such as a VIP1A(a) protein or a VIP1A(b) protein, or a VIP2-type protein, such as a VIP2A(a) protein or a VIP2A(b) protein or a combination of a VIP1-type protein and a VIP2-type protein.
7. A method according to claim 1, wherein the toxin protein is a VIP3-type protein, such as a VIP3A(a) protein or a VIP3A(b) protein.
8. A method according to anyone of claims 6 to 7, wherein the toxin protein is a VIP-type protein according to SEQ ID Nos. 1, 2, 4-7, 17-24, 26-32, 35, 36, 39, 40, 42, 43, 45, 46, 49, 50, 51 or 52.

9. The method according to claim 1, wherein the toxin protein is applied to the plant in form of an entomocidal composition.
10. The method according to claim 9, wherein the entomocidal composition comprises a microorganism.
11. The method according to claim 1 or 9, wherein the toxin protein is a CryI-type protein.
12. The method according to claim 9, wherein the entomocidal composition comprises at least one CryI-type toxin protein or a microorganism, preferably a *Bacillus thuringiensis* and/or a *Bacillus cereus* strain, containing at least one gene encoding said toxin protein together with a suitable carrier.
13. The method according to claim 12, wherein the microorganism is a naturally-occurring organism containing at least one *cryI*-type toxin gene encoding said toxin protein.
14. A method according to claim 10, wherein the microorganism is a naturally-occurring organism containing at least one *cry*-type toxin gene, preferably a *cryI*-type toxin gene, more preferably a *cryIA*-type toxin gene, and most preferably a *cryIA(b)* toxin gene.
15. The method according to claim 12, wherein the microorganism is a recombinant organism containing at least one *cryI*-type toxin gene in recombinant form encoding said toxin protein.
16. A method according to claim 10, wherein the microorganism is a recombinant organism containing at least one *cry*-type toxin gene, preferably a *cryI*-type toxin gene, more preferably a *cryIA*-type toxin gene, and most preferably a *cryIA(b)* toxin gene.

17. The method according to claim 10, wherein the entomocidal composition comprises at least one VIP-type toxin protein or a microorganism, preferably a *Bacillus thuringiensis* and/or a *Bacillus cereus* strain, containing at least one gene encoding said toxin protein together with a suitable carrier.
18. A method according to claim 10, wherein the microorganism is a naturally-occurring organism containing at least one VIP-type protein gene encoding the said toxin protein, preferably a VIP1A(a) protein or a VIP1A(b) protein gene or a VIP2-type protein gene such as a VIP2A(a) protein or a VIP2A(b) protein gene.
19. A method according to claim 10, wherein the microorganism is a naturally-occurring organism containing at least one VIP3-type protein gene such as a VIP3A(a) protein or a VIP3A(b) protein gene encoding the said toxin protein.
20. A method according to anyone of claims 17-19, wherein the toxin protein is a VIP-type protein according to SEQ ID Nos. 1, 2, 4-7, 17-24, 26-32, 35, 36, 39, 40, 42, 43, 45, 46, 49, 50, 51 or 52.
21. A method according to anyone of claims 11-16, wherein the toxin protein is a Cry-type protein according to SEQ ID Nos. 53 to 55.
22. Anyone of claims 17 to 21, wherein the microorganism is a recombinant organism.
23. The method according to claim 1 to 22, wherein the toxin protein is indirectly applied to the plant, by transforming said plant with a toxin gene encoding a toxin protein of *Bacillus species* and expressing said toxin protein in an amount sufficient to provide control against *Ostrinia furnacalis* (*Asian Corn Borer*) species upon planting the so transformed plant in an area where said insect pest may occur.
24. A method according to claim 23, wherein the toxin gene encodes a toxin protein of *Bacillus thuringiensis* or *Bacillus cereus*.

25. A method according to claim 23, wherein the toxin gene encodes a Cry-type toxin protein, preferably a CryI-type protein, more preferably a CryIA-type protein, and most preferably a CryIA(b) protein such as those provided in SEQ ID Nos. 53 to 55.

26. A method according to claim 23, wherein the toxin gene encodes a VIP-type toxin protein, preferably a VIP1-type protein, such as a VIP1A(a) protein or a VIP1A(b) protein or a VIP2-type protein, such as a VIP2A(a) protein or a VIP2A(b) protein.

27. A method according to claim 23, wherein the toxin gene encodes a VIP3-type protein, such as as a VIP3A(a) protein or a VIP3A(b) protein.

28. The method according to claim 23-27, wherein the toxin gene is a synthetic gene the codon usage of which is optimized by using the codons which are most preferred in plants.

29. The method according to claims 23 and 28, wherein the toxin gene encodes a CryI-type protein.

30. A method according to any one of claims 26 to 27, wherein the toxin gene encodes a VIP-type protein according to SEQ ID Nos. 1, 2, 4-7, 17-24, 26-32, 35, 36, 39, 40, 42, 43, 45, 46, 49, 50, 51 or 52.

31. The method according to any one of claims 1 to 30, wherein the plant to be protected is a cereal plant.

32. The method according to claim 31, wherein the plant to be protected is a maize plant.

33. A method according to any one of claims 1 to 32, wherein at least a Cry-type toxin protein is directly or indirectly applied to the plant or the plant seed or the growing area of

the plant to be protected in combination with a VIP-type toxin protein in an amount sufficient to provide control against Asian Corn Borer (*Ostrinia furnacalis*) pests.

34. The method according to any one of claims 1 to 32, wherein the active ingredient is a CryIA(b) protein.

35. The method according to any one of claims 1 to 32, wherein the active ingredient is a VIP-type protein.

36. Use of an active ingredient as defined in the previous claims for controlling *Ostrinia furnacalis* (Asian Corn Borer) pests in crop plants.

37. Use of a transgenic plant as defined in claim 23 for controlling *Ostrinia furnacalis* (Asian Corn Borer) pests in crop plants.

38. Use of recombinant microorganisms or transgenic plants according to anyone of claims 23 to 30 comprising a DNA molecule which hybridizes to a cry-type or a VIP-type gene encoding the respective toxin protein under moderate stringent conditions for controlling *Ostrinia furnacalis* (Asian Corn Borer) pests in crop plants.

39. A commercial bag comprising seed of a transgenic plant comprising a toxin gene encoding a toxin protein of *Bacillus thuringiensis* and expressing said toxin protein in an amount sufficient to provide control against *Ostrinia furnacalis* (Asian Corn Borer) species, together with label instructions for the use thereof for control of *Ostrinia furnacalis* (Asian Corn Borer) pests in crop plants.

40. A commercial bag comprising seed of a transgenic plant or a microorganism, but especially a *Bacillus thuringiensis* and/or a *Bacillus cereus* strain, comprising at least a toxin gene encoding a toxin protein as defined previously in claims 1 to 30, 32 and 33, and expressing the said toxin protein in an amount sufficient to provide control against *Ostrinia furnacalis* (Asian Corn Borer) species, together with label instructions for the use thereof for

control of *Ostrinia furnacalis* (*Asian Corn Borer*) pests in crop plants.

41. An agricultural method, wherein a transgenic plant or the progeny thereof is used comprising a toxin gene encoding a toxin protein of a *Bacillus species* and expressing the said toxin protein in an amount sufficient to provide control against *Ostrinia furnacalis* (*Asian Corn Borer*) species or transgenic seed thereof, as defined in anyone of claims 23 to 32.

42. A method according to any one of claims 18 to 26, wherein at least a Cry-type toxin protein is expressed in the plant to be protected in combination with a VIP-type toxin protein in an amount sufficient to provide control against *Sesamia* pests.

43. A composition comprising as an active ingredient at least a Cry-type toxin protein and a VIP-type protein in a insecticidally effective amount together with a agronomically acceptable carrier.

## INTERNATIONAL SEARCH REPORT

Int onal Application No

PCT/EP 97/02737

A. CLASSIFICATION OF SUBJECT MATTER  
 IPC 6 A01N63/02 A01N63/00

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 A01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No.                                       |
|------------|------------------------------------------------------------------------------------|-------------------------------------------------------------|
| E          | WO 97 26339 A (NOVARTIS AG) 24 July 1997<br>see the whole document                 | 1-35,<br>39-43                                              |
| X          | EP 0 589 110 A (PLANT GENETIC SYSTEMS<br>N.V.) 30 March 1994                       | 1,2,4,5,<br>9-16,<br>21-25,<br>28,29,<br>31,32,<br>34,36-41 |
| Y          | see the whole document                                                             | 3,6-8,<br>17-20,<br>26,27,<br>30,33,<br>35,42,43            |

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

## \* Special categories of cited documents:

- \*A\* document defining the general state of the art which is not considered to be of particular relevance
- \*E\* earlier document but published on or after the international filing date
- \*L\* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- \*O\* document referring to an oral disclosure, use, exhibition or other means
- \*P\* document published prior to the international filing date but later than the priority date claimed

- \*T\* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- \*X\* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- \*Y\* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
- \*A\* document member of the same patent family

Date of the actual completion of the international search

18 September 1997

Date of mailing of the international search report

06-10-1997

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2  
 NL - 2280 HV Rijswijk  
 Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,  
 Fax: (+31-70) 340-3016

Authorized officer

Muellners, W



## INTERNATIONAL SEARCH REPORT

In International Application No  
PCT/EP 97/02737

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages                                                                                                                                                                                                                                                                                                                  | Relevant to claim No.                            |
|------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------|
| Y          | WO 96 10083 A (CIBA-GEIGY AG) 4 April 1996<br><br>see the whole document<br>---                                                                                                                                                                                                                                                                                                                     | 3,6-8,<br>17-20,<br>26,27,<br>30,33,<br>35,42,43 |
| X          | I.H.SCHREINER ET AL.: "Detasseling and<br>Insecticides for Control of Ostrinia<br>furnacalis (Lepidoptera: Pyralidae) on<br>Sweet Corn"<br>JOURNAL OF ECONOMIC ENTOMOLOGY,<br>vol. 80, no. 1, February 1987, COLLEGE<br>PARK, MD, US,<br>pages 263-267, XP002041102<br>see the whole document<br>---                                                                                                | 1,2,4,<br>9-14,31,<br>32,34,36                   |
| X          | DATABASE BIOSIS<br>BIOSCIENCES INFORMATION SERVICE,<br>PHILADELPHIA, PA, US<br>CHENG W Y ET AL: "The pathogenicity of<br>Bacillus thuringiensis var. kurstaki to<br>the 4th instar larvae of Asian corn borer,<br>Ostrinia furnacalis, in the laboratory."<br>XP002041104<br>see abstract<br>&<br>REPORT OF THE TAIWAN SUGAR RESEARCH<br>INSTITUTE 0 (149). 1995. 13-19. ISSN:<br>0257-5493,<br>--- | 1,2,4,<br>9-14,31,<br>32,34,36                   |
| X          | DATABASE BIOSIS<br>BIOSCIENCES INFORMATION SERVICE,<br>PHILADELPHIA, PA, US<br>CHENG W Y ET AL: "Biological control of<br>Asian corn borer in sweet corn fields."<br>XP002041105<br>see abstract<br>&<br>REPORT OF THE TAIWAN SUGAR RESEARCH<br>INSTITUTE 0 (148). 1995. 11-29. ISSN:<br>0257-5493,<br>---                                                                                          | 1,2,4,<br>9-14,31,<br>32,34,36                   |
| X          | DATABASE BIOSIS<br>BIOSCIENCES INFORMATION SERVICE,<br>PHILADELPHIA, PA, US<br>SUN LIANGWU ET AL: "Construction of<br>shuttle vector containing delta-endotoxin<br>gene of Bacillus thuringiensis."<br>XP002041106<br>see abstract<br>&<br>WEISHENGWU XUEBAO 36 (1). 1996. 69-72.<br>ISSN: 0001-6209,<br>---                                                                                        | 1-4,<br>9-12,<br>15-17,<br>22,33,<br>36,38       |
|            | ---                                                                                                                                                                                                                                                                                                                                                                                                 |                                                  |

-/--

## INTERNATIONAL SEARCH REPORT

Int .ional Application No

PCT/EP 97/02737

| C(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                                                                                                 |
|-----------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------|
| Category *                                          | Citation of document, with indication, where appropriate, of the relevant passages                                                                                                                                                                                                                                                                                                                                                                                                                          | Relevant to claim No.                                                                                                                           |
| X                                                   | <p>DATABASE CHEMABS<br/>           CHEMICAL ABSTRACTS SERVICE, COLUMBUS,<br/>           OHIO, US<br/>           CHEN, QI ET AL: "Molecular cloning and<br/>           expression of Bacillus thuringiensis<br/>           subsp. galleriae insecticidal crystal<br/>           protein genes in Escherichia coli"<br/>           XP002041107<br/>           see abstract<br/>           &amp;<br/>           SCI. CHINA, SER. B (1989), 32(7), 830-6<br/>           CODEN: SCBSE5,<br/>           1989,</p> | <p>1-4,<br/>           9-12,<br/>           15-17,<br/>           22,33,<br/>           36,38</p>                                               |
| X                                                   | <p>DATABASE CHEMABS<br/>           CHEMICAL ABSTRACTS SERVICE, COLUMBUS,<br/>           OHIO, US<br/>           DING, QUN-XING ET AL: "Introducing Bt gene<br/>           into maize with ovary injection"<br/>           XP002041108<br/>           see abstract<br/>           &amp;<br/>           SCI. CHINA, SER. B (1994), 37(5), 563-72<br/>           CODEN: SCBSE5;ISSN: 1001-652X,<br/>           1994,</p>                                                                                       | <p>1,2,4,5,<br/>           11,<br/>           23-25,<br/>           28,29,<br/>           31,32,<br/>           34,<br/>           36-38,41</p> |
| X                                                   | <p>M.G.KOZIEL ET AL.: "Field Performance of<br/>           Elite Transgenic Maize Plants Expressing<br/>           an Insecticidal Protein Derived from<br/>           Bacillus thuringiensis"<br/>           BIO/TECHNOLOGY,<br/>           vol. 11, February 1993, NEW YORK,US,<br/>           pages 194-200, XP002029715<br/>           see the whole document</p>                                                                                                                                       | <p>1,2,4,5,<br/>           11,<br/>           23-25,<br/>           28,29,<br/>           31,32,<br/>           34,41</p>                       |
| A                                                   | <p>H.HÖFTE &amp; H.R.WHITELEY: "Insecticidal<br/>           Crystal Proteins of Bacillus<br/>           thuringiensis"<br/>           MICROBIOLOGICAL REVIEWS,<br/>           vol. 53, no. 2, June 1989, WASHINGTON, DC,<br/>           US,<br/>           pages 242-55, XP002041103<br/>           see the whole document</p>                                                                                                                                                                              | <p>1-43</p>                                                                                                                                     |

# INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/EP 97/02737

| Patent document<br>cited in search report | Publication<br>date | Patent family<br>member(s) | Publication<br>date |
|-------------------------------------------|---------------------|----------------------------|---------------------|
| WO 9726339 A                              | 24-07-97            | NONE                       |                     |
| EP 589110 A                               | 30-03-94            | US 5628995 A               | 13-05-97            |
|                                           |                     | US 5530197 A               | 25-06-96            |
| WO 9610083 A                              | 04-04-96            | AU 3743395 A               | 19-04-96            |
|                                           |                     | CA 2199049 A               | 04-04-96            |
|                                           |                     | EP 0792363 A               | 03-09-97            |
|                                           |                     | ZA 9508121 A               | 29-04-96            |

**This Page is Inserted by IFW Indexing and Scanning  
Operations and is not part of the Official Record**

**BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☐ FADED TEXT OR DRAWING
- ☐ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☒ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☒ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: \_\_\_\_\_

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.**